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CONTINUATION-IN-PART APPLICATION

TRANSMITTAL

Sir:

Transmitted herewith for filing is a **Continuation-in-Part** of International Application No. PCT/US99/07333 which claims the benefit of U.S. Application No. 60/080,671, Filed April 3, 1998.

Inventor(s): **Thomas Stormann, Lance G. Hammerland, Laura L. Storjohann, James G. Busby, James E. Garrett, Rachel T. Simin**

Title: **G-PROTEIN FUSION RECEPTORS AND CHIMERIC $GABA_B$ RECEPTORS**

I. PAPERS ENCLOSED HEREWITH FOR FILING UNDER 37 CFR § 1.53(b):

33 Page(s) of Written Description

7 Page(s) Claims

1 Page(s) Abstract

102 Other: Sequence Listing

116 Sheets of Drawings ______ Informal X_____ Formal

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CONTINUATION-IN-PART APPLICATION

UNDER 37 CFR § 1.53(B)

TITLE: G-PROTEIN FUSION RECEPTORS AND CHIMERIC $GABA_B$ RECEPTORS

APPLICANT(S): Thomas Stormann, Lance G. Hammerland, Laura L. Storjohann, James G. Busby, James E. Garrett, Rachel T. Simin

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G-PROTEIN FUSION RECEPTORS AND CHIMERIC $GABA_B$ RECEPTORS

RELATED APPLICATIONS

The present application is a continuation in part of PCT/US99/07333 which claims priority to Garrett *et al.* U.S. Serial No. 60/080,671, filed April 3, 1998, which is hereby incorporated by reference herein in its entirety including the drawings.

FIELD OF THE INVENTION

The present invention relates to a G-protein fusion receptors, chimeric $GABA_B$ (γ-aminobutyric acid) receptors, nucleic acid encoding such receptors, and uses of such receptors and nucleic acid encoding such receptors.

BACKGROUND

The references cited herein are not admitted to be prior art to the claimed invention.

Chimeric receptors made up of peptide segments from different receptors have different uses such as being used to assess the functions of different sequence regions and to assess the activity of different compounds at a particular receptor. Examples of using chimeric receptors to assess the activity of different compounds are provided by Dull *et al.,* U.S. Patent No. 4,859,609, Dull *et al.,* U.S. Patent No. 5,030,576, and Fuller *et al.,* U.S. Patent No. 5,981,195.

Dull *et al.* U.S. Patent No. 4,859,609, and Dull *et al.* U.S. Patent No. 5,030,576, indicate the production and use of chimeric receptors comprising a ligand binding domain of a predetermined receptor and a heterologous reporter polypeptide. The Dull *et al.* patents provide as examples of chimerics: (1) a chimeric receptor made up of the insulin receptor extracellular chain, and the EGF receptor transmembrane and cytoplasmic domains without any HIR B-chain sequence; and (2) a hybrid receptor made up of the v-erB oncogene product intracellular domain fused to the EGF receptor extracellular and transmembrane domains.

Fuller *et al.* International Publication No. WO 97/05252 feature chimeric receptors made up of metabotropic glutamate receptor (mGluR) domains and calcium receptor

(CaR) domains. The chimeric receptors allow the coupling of functional aspects of a mGluR with a CaR.

An example of the use of chimeric receptors to assess the functions of different sequence regions receptors are found in studies identifying regions of different guanine nucleotide-binding protein coupled receptors important for guanine nucleotide-binding protein coupling. (See, Kobilka *et al.*, *Science 240*:1310-1316, 1988; Wess *et al.*, *FEBS Lett. 258*:133-136, 1989; Cotecchia *et al.*, *Proc. Natl. Acad. Sci. USA 87*:2896-2900, 1990; Lechleiter *et al.*, *EMBO J. 9*:4381-4390, 1990; Wess *et al.*, *Mol. Pharmacol. 38*:517-523, 1990; and Pin *et al.*, *EMBO J. 13*:342-348, 1994.)

SUMMARY OF THE INVENTION

The present invention features G-protein fusion receptors and chimeric $GABA_B$ receptors ($GABA_BRs$), nucleic acid encoding such receptors, and the use of such receptors and nucleic acid. G-protein fusion receptors comprise at least one domain from a CaR, a mGluR, and/or a $GABA_B$ receptor fused directly or through a linker to a guanine nucleotide-binding protein (G-protein). Chimeric $GABA_BRs$ comprise at least one of a $GABA_BR$ extracellular domain, a $GABA_BR$ transmembrane domain, or a $GABA_BR$ intracellular domain and one or more domains from a mGluR subtype 8 (mGluR8) and/or a CaR.

G-proteins are peripheral membrane proteins made up of an subunit, a subunit, and a subunit. G-proteins interconvert between a GDP bound and a GTP bound form. Different types of G-proteins can affect different enzymes, such as adenylate cyclase and phospholipase-C.

Thus, a first aspect of the present invention describes a G-protein fusion receptor comprising:

an extracellular domain comprising an amino acid sequence substantially similar to either an extracellular CaR amino acid sequence, an extracellular mGluR amino acid sequence, or an extracellular $GABA_B$ receptor amino acid sequence;

a transmembrane domain joined to the carboxy terminus of said extracellular domain, said transmembrane domain comprising a transmembrane domain amino acid sequence substantially similar to either a transmembrane CaR amino acid sequence, a transmembrane mGluR amino acid sequence, or a transmembrane $GABA_B$ receptor amino acid sequence;

an intracellular domain joined to the carboxy terminus of said transmembrane domain comprising all or a portion of an intracellular amino acid sequence substantially similar to either an intracellular CaR amino acid sequence, an intracellular mGluR amino acid sequence, or an intracellular $GABA_B$ receptor amino acid sequence, provided that said portion is at least about 10 amino acids;

an optionally present linker joined to the carboxy terminus of said intracellular domain, where said optionally present linker is a polypeptide 3 to 30 amino acids in length, wherein said amino acids of the optionally present linker are selected from the group consisting of alanine, proline, serine, and glycine; and

a G-protein joined either to said intracellular domain or to said optionally present linker, provided that said G-protein is joined to said optionally present linker when said optionally present linker is present.

"Substantially similar" refers to at least 40% sequence similarity between respective polypeptide regions making up a domain. In preferred embodiments, substantially similar refers to at least 50%, at least 75%, at least 90%, at least 95% sequence similarity, or 100% (the same sequence), between polypeptide domains. The degree to which two polypeptide domains are substantially similar is determined by comparing the amino acid sequences located in corresponding domains. Sequence similarity is preferably determined using BLASTN (Altschul *et al., J. Mol. Biol. 215:*403-410, 1990).

The different receptor components of the G-protein receptor can come from the same receptor protein or from a chimeric receptor made up of different receptor domains. By swapping different domains compounds able to effect different domains of a particular receptor can be identified and the activity of different compounds at different domains can be measured.

In different embodiments the CaR region(s) present in the G-protein fusion are substantially similar to, comprise, or consist of portion(s) of a mammalian CaR, preferably the human CaR; mGluR region(s) present in the G-protein fusion are substantially similar to, comprise, or consist of portion(s) of a mammalian mGluR, preferably a human mGluR; and $GABA_BR$ region(s) present in the G-protein fusion are substantially similar to, comprise, or consist of portion(s) of a mammalian $GABA_BR$, preferably a human $GABA_BR$.

In preferred embodiments concerning $GABA_BR$ regions that are present: the $GABA_BR$ extracellular domain is substantially similar to a $GABA_BR$ extracellular domain provided in SEQ. ID. NOs. 2-4; the $GABA_BR$ transmembrane domain is substantially similar to the $GABA_BR$ transmembrane domain provided in SEQ. ID. NOs. 7-9; and the $GABA_BR$ intracellular domain is substantially similar to a $GABA_BR$ intracellular domain provided in SEQ. ID. NOs. 12-14.

In preferred embodiments concerning CaR regions that are present: the CaR extracellular domain is substantially similar to the CaR extracellular provided in SEQ. ID. NO. 1; the CaR transmembrane domain is substantially similar to the CaR transmembrane domain provided in SEQ. ID. NO. 6; and the CaR intracellular domain is substantially similar to the CaR intracellular domain such as that provided in SEQ. ID. NO. 11.

Various different mGluR subtypes present in different organisms, including humans, are described in different patent publications as follows: $mGluR_1$ - WO 94/29449, EP 569 240 A1, WO 92/10583 and U.S. Patent No. 5,385,831; $mGluR_2$ - WO 94/29449, WO 96/06167, and EP 711 832 A2; $mGluR_3$ - WO 94/29449, and WO 95/22609; $mGluR_4$ – WO 95/08627, WO 95/22609, and WO 96/29404; $mGluR_5$ - WO 94/29449; $mGluR_6$ - WO 95/08627; $mGluR_7$ – U.S. Patent No. 5,831,047, WO 95/08627 and WO 96/29404; and $mGluR_8$ – U.S. Patent Nos. 6,051,688, 6,077,675, 6,084,084 and EP 816 498 A2. (Each of these references are hereby incorporated by reference herein.)

In preferred embodiments concerning mGluR regions that are present: the mGluR extracellular domain is substantially similar to either human mGluR 1, human mGluR 2, human mGluR 3, human mGluR 4, human mGluR 5, human mGluR 6, human mGluR 7, or human mGluR 8; the mGluR transmembrane domain is substantially similar to either human mGluR 1, human mGluR 2, human mGluR 3, human mGluR 4, human mGluR 5, human mGluR 6, human mGluR 7, or human mGluR 8; and the mGluR intracellular domain is substantially similar to either human mGluR 1, human mGluR 2, human mGluR 3, human mGluR 4, human mGluR 5, human mGluR 6, human mGluR 7, or human mGluR 8. Preferred embodiments also include any mGluR splice variant.

In preferred embodiments concerning the optionally present linker, said optionally present linker is a polypeptide 3 to 30 amino acids in length, wherein said amino acids of the optionally present linker are selected from the group consisting of alanine, proline, serine, and glycine; and more preferably, the optionally present linker is comprised of alanine amino acids.

Another aspect of the present invention describes a recombinant cell comprising an expression vector encoding for a G-protein fusion receptor, and a cell where the G-protein fusion receptor is expressed. Preferably, the G-protein fusion receptor is functional in the cell.

Another aspect of the present invention describes a recombinant cell produced by combining (a) a cell where a G-protein fusion receptor is expressed, and (b) a vector comprising nucleic acid encoding a G-protein fusion receptor and elements for introducing heterologous nucleic acid into the cell. Preferably, the G-protein fusion receptor is functional in the cell.

Another aspect of the present invention describes a process for the production of a G-protein fusion receptor. The process is performed by growing host cells comprising a G-protein fusion receptor.

Another aspect of the present invention describes a method of measuring the ability of a compound to affect G-protein fusion receptor activity.

Another aspect of the present invention describes a chimeric $GABA_BR$ comprising an extracellular domain, a transmembrane domain and an intracellular domain, wherein at least one domain is from a $GABA_BR$ and at least one domain is from CaR or mGluR8. The extracellular domain comprises an amino acid sequence substantially similar to a CaR extracellular domain (SEQ. ID. NO. 1), a $GABA_BR1a$ extracellular domain (SEQ. ID. NO. 2), a $GABA_BR1b$ extracellular domain (SEQ. ID. NO. 3), a $GABA_BR2$ extracellular domain (SEQ. ID. NO. 4), or a mGluR8 extracellular domain (SEQ. ID. NO. 5).

The transmembrane domain comprises an amino acid sequence substantially similar to a CaR transmembrane domain (SEQ. ID. NO. 6), a $GABA_BR1a$ transmembrane domain (SEQ. ID. NO. 7), a $GABA_BR1b$ transmembrane domain (SEQ. ID. NO. 8), a $GABA_BR2$ transmembrane domain (SEQ. ID. NO. 9), or a mGluR8 transmembrane domain (SEQ. ID. NO. 10).

The intracellular domain comprises an amino acid sequence substantially similar to a CaR intracellular domain (SEQ. ID. NO. 11), a $GABA_BR1a$ intracellular domain (SEQ. ID. NO. 12), a $GABA_BR1b$ intracellular domain (SEQ. ID. NO. 13), a $GABA_BR2$ intracellular domain (SEQ. ID. NO. 14), or a mGluR8 intracellular domain (SEQ. ID. NO. 15).

Preferred chimeric $GABA_BRs$ contain at least one mGluR8 intracellular, transmembrane or extracellular domain, or at least one CaR intracellular, transmembrane or extracellular domain. More preferably, the chimeric $GABA_BR$ contains at least one CaR domain.

In preferred embodiments concerning mGluR8 regions that are present: the mGluR8 extracellular domain is substantially similar to the mGluR8 extracellular domain provided in SEQ. ID. NO. 5; the mGluR8 transmembrane domain is substantially similar to the mGluR8 transmembrane domain provided in SEQ. ID. NO. 10; and the mGluR8 intracellular domain is substantially similar to the mGluR8 receptor intracellular provided in SEQ. ID. NO. 15.

Preferably, the domains are functionally coupled such that a signal from the binding of an extracellular ligand is transduced to the intracellular domain when the chimeric receptor is present in a suitable host cell. A suitable host cell contains the elements for functional signal transduction for receptors coupled to a G-protein.

Another aspect of the present invention describes a nucleic acid comprising a nucleotide sequence encoding for a chimeric $GABA_BR$.

Another aspect of the present invention describes a recombinant cell comprising an expression vector encoding for a chimeric $GABA_BR$, and a cell where the chimeric $GABA_BR$ is expressed. Preferably, the chimeric $GABA_BR$ is functional in the cell.

Another aspect of the present invention describes a recombinant cell produced by combining (a) a cell where a chimeric $GABA_BR$ is expressed, and (b) a vector comprising nucleic acid encoding the chimeric $GABA_BR$ and elements for introducing heterologous nucleic acid into the cell. Preferably, the chimeric $GABA_BR$ is functional in the cell.

Another aspect of the present invention describes a process for the production of a chimeric receptor. The process is performed by growing host cells comprising a chimeric $GABA_BR$.

Another aspect of the present invention describes a method of measuring the ability of a compound to affect $GABA_BR$ or mGluR activity. The method is performed by measuring the ability of a compound to affect chimeric $GABA_BR$ or mGluR activity.

Another aspect of the present invention describes a fusion receptor polypeptide comprising a receptor and a G-protein α subunit, wherein said G-protein α subunit is fused to the intracellular domain of said receptor, provided that the receptor is not an adrenoreceptor.

Various examples are described herein. These examples are not intended in any way to limit the claimed invention.

Other features and advantages of the invention will be apparent from the following drawings, the description of the invention, the examples, and the claims.

BRIEF DESCRIPTION OF DRAWINGS

Figures 1a-1d illustrate the amino acid sequences of a human CaR extracellular domain (SEQ. ID. NO. 1), a human $GABA_BR1a$ extracellular domain (SEQ. ID. NO. 2), a human $GABA_BR1b$ extracellular domain (SEQ. ID. NO. 3), a human $GABA_BR2$ extracellular domain (SEQ. ID. NO. 4), and a human mGluR8 extracellular domain (SEQ. ID. NO. 5).

Figures 2a-2b illustrate the amino acid sequences of a human CaR transmembrane domain (SEQ. ID. NO. 6), a human $GABA_BR1a$ transmembrane domain (SEQ. ID. NO. 7), a human $GABA_BR1b$ transmembrane domain (SEQ. ID. NO. 8), a human $GABA_BR2$ transmembrane domain (SEQ. ID. NO. 9), and a human mGluR8 transmembrane domain (SEQ. ID. NO. 10).

Figures 3a-3b illustrate the amino acid sequences of a human CaR intracellular domain (SEQ. ID. NO. 11), a human $GABA_BR1a$ intracellular domain (SEQ. ID. NO. 12), a human $GABA_BR1b$ intracellular domain (SEQ. ID. NO. 13), a human $GABA_BR2$ intracellular domain (SEQ. ID. NO. 14), and a human mGluR8 intracellular domain (SEQ. ID. NO. 15).

Figures 4a-4b illustrate the amino acid sequence of G_{15} (SEQ. ID. NO. 16) and G_{16} (SEQ. ID. NO. 17).

Figures 5a-5r illustrate the cDNA sequences encoding for human CaR (SEQ. ID. NO. 18), human $GABA_BR1a$ (SEQ. ID. NO. 19), human $GABA_BR1b$ (SEQ. ID. NO. 20), and human $GABA_BR2$ (SEQ. ID. NO. 21).

Figures 6a-6h illustrate the cDNA sequence for rat $GABA_BR1a$ (SEQ. ID. NO. 22) and rat $GABA_BR1b$ (SEQ. ID. NO. 23).

Figures 7a-7c illustrate the amino sequence for rat $GABA_BR1a$ (SEQ. ID. NO. 24) and rat $GABA_BR1b$ (SEQ. ID. NO. 25).

Figure 8 illustrates the ability of a chimeric CaR/$GABA_BR2$ (CaR extracellular and transmembrane domains, and intracellular $GABA_BR2$ domain) to transduce a signal. Signal production was measured by detecting an increase in the calcium-activated

chloride current. The line in the middle of the increase signifies a wash step.

Figures 9a-9p illustrate the cDNA sequence for human mGluR2 (SEQ. ID. NO. 26), chimeric hCAR/hmGluR2 (SEQ. ID. NO. 30), chimeric hmGluR2/hCaR (SEQ. ID. NO. 34), and chimeric hmGluR8/hCaR (SEQ. ID. NO. 38).

Figures 10a-10f illustrate the amino acid sequence for human mGluR2 (SEQ. ID. NO. 27), chimeric hCAR/hmGluR2 (SEQ. ID. NO. 31), chimeric hmGluR2/hCaR (SEQ. ID. NO. 35), chimeric hmGluR8/hCaR (SEQ. ID. NO. 39).

Figures 11a-11v illustrate the cDNA sequence for the phCaR/hmGluR2*Gqi5 fusion construct (SEQ. ID. NO. 32), pmGluR2//CaR*G $_q$i5 fusion construct (SEQ. ID. NO. 36), pmGluR2//CaR*G $_q$i5+3Ala linker fusion construct (SEQ. ID. NO. 46), and the mGluR8//CaR*G $_q$i5 fusion construct (SEQ. ID. NO. 40).

Figures 12a-12h illustrate the amino acid sequence for the phCaR/hmGluR2*Gqi5 fusion construct (SEQ. ID. NO. 33), pmGluR2//CaR*G $_q$i5 fusion construct (SEQ. ID. NO. 37), pmGluR2//CaR*G $_q$i5+3Ala linker fusion construct (SEQ. ID. NO. 47), and the mGluR8//CaR*G $_q$i5 fusion construct (SEQ. ID. NO. 41).

Figures 13a-13m illustrate the cDNA sequence for the GABA-R2*Gqo5 fusion construct (SEQ. ID. NO. 42) and the GABA-BR1a*Gqo5 fusion construct (SEQ. ID. NO. 44).

Figures 14a-14e illustrates the amino acid sequence for the GABA-BR2*Gqo5 fusion construct (SEQ. ID. NO. 43) and the GABA-BR1a*Gqo5 fusion construct (SEQ. ID. NO. 45).

Figure 15 illustrates the ability of different G-protein fusions to transduce signal resulting from ligand binding. mGluR2//CaR*Gqi5 is shown by SEQ. ID. NO. 37, CaR/mGluR2*Gqi5 is shown by SEQ. ID. NO. 33, mGluR8//CaR*Gqi5 is shown by SEQ. ID. NO. 41.

Figures 16a-16e illustrates the amino acid sequence for the ph8SPmGluR4 chimeric construct (SEQ. ID. NO.48), the amino acid sequence for the phmGluR4//CaR*AAA*Gα_qi5 fusion construct (SEQ. ID. NO. 49), and the phmGluR8//CaR*AAA*Gα_qi5 fusion construct (SEQ. ID. NO. 50).

DETAILED DESCRIPTION OF THE INVENTION

The CaR, mGluR, and the $GABA_BR$ are structurally similar in that they are each a single subunit membrane protein possessing an extracellular domain, a transmembrane domain comprising seven putative membrane spanning helices connected by three intracellular and three extracellular loops, and an intracellular carboxy-terminal domain. Signal transduction is activated by the extracellular binding of an agonist. The signal is transduced to the intracellular components of the receptor causing an intracellular effect.

Signal transduction from agonist binding to an extracellular region can be modulated by compounds acting at a downstream transmembrane domain or the intracellular domain. Downstream effects include antagonist actions of compounds and allosteric actions of compounds.

The transmembrane domain provides different types of target sites for compounds modulating receptor activity in different environments. As noted above, the transmembrane domain contains extracellular, transmembrane, and intracellular components.

Compounds modulating $GABA_BR$, CaR, or mGluR activity can be obtained, for example, by screening a group or library of compounds to identify those compounds having the desired activity and then synthesizing such compound. Thus, included in the present invention is a method of making a $GABA_BR$, CaR, or mGluR active compound by first screening for a compound having desired properties and then chemically synthesizing that compound.

Metabotropic Glutamate Receptors (mGluRs)

mGluRs are G protein-coupled receptors capable of activating a variety of intracellular secondary messenger systems following the binding of glutamate (Schoepp *et al.*, *Trends Pharmacol. Sci. 11*:508, 1990; Schoepp and Conn, *Trends Pharmacol. Sci. 14*:13, 1993, hereby incorporated by reference herein).

Activation of different mGluR subtypes *in situ* elicits one or more of the following responses: activation of phospholipase C, increases in phosphoinositide (PI) hydrolysis, intracellular calcium release, activation of phospholipase D, activation or inhibition of adenylyl cyclase, increases and decreases in the formation of cyclic adenosine monophosphate (cAMP), activation of guanylyl cyclase, increases in the formation of cyclic guanosine monophosphate (cGMP), activation of phospholipase A_2, increases in arachidonic acid release, and increases or decreases in the activity of voltage- and ligand-

gated ion channels (Schoepp and Conn, *Trends Pharmacol. Sci.* 14:13, 1993; Schoepp, *Neurochem. Int.* 24:439, 1994; Pin and Duvoisin, *Neuropharmacology* 34:1, 1995, hereby incorporated by reference herein).

Eight distinct mGluR subtypes have been isolated. (Nakanishi, *Neuron* 13:1031, 1994; Pin and Duvoisin, *Neuropharmacology* 34:1, 1995; Knopfel et al., *J. Med. Chem.* 38:1417; *Eur. J. Neuroscience* 7:622-629, 1995, each of these references is hereby incorporated by reference herein.) The different mGluRs possess a large amino-terminal extracellular domain (ECD) followed by a seven putative transmembrane domain (7TMD) comprising seven putative membrane spanning helices connected by three intracellular and three extracellular loops, and an intracellular carboxy-terminal domain of variable length (cytoplasmic tail).

Human mGluR8 is described by Stormann *et al.,* U.S. Patent Nos. 6,051,688, 6,077,675, and 6,084,084, and mouse mGluR8 is described by *Duvoisin et al.*, *J. Neurosci.* 15:3075-3083, 1995, (both of these references are hereby incorporated by reference herein). mGluR8 couples to G_i. Agonists of mGluR8 include L-glutamate and L-2-amino-4-phosphonobutyrate.

mGluR8 activity can be measured using standard techniques. For example, G_i negatively couples to adenylate cyclase to inhibit intracellular cAMP accumulation in a pertussis toxin-sensitive fashion. Thus, mGluR8 activity can be measured, for example, by measuring inhibition of forskolin-stimulated cAMP production as described by *Duvoisin et al., J. Neurosci.* 15:3075-3083, 1995.

mGluRs have been implicated in a variety of neurological pathologies. Examples of such pathologies include stroke, head trauma, spinal cord injury, epilepsy, ischemia, hypoglycemia, anoxia, and neurodegenerative diseases such as Alzheimer's disease (Schoepp and Conn, *Trends Pharmacol. Sci. 14*:13, 1993; Cunningham *et al.*, *Life Sci.* 54: 135, 1994; Pin et al., *Neuropharmacology* 34:1, 1995; Knopfel et al., *J. Med. Chem.* 38:1417, 1995, each of which is hereby incorporated by reference herein).

Calcium Receptor

The CaR responds to changes of extracellular calcium concentration and also responds to other divalent and trivalent cations. The CaR is a G-protein coupled receptor containing an extracellular Ca^{2+} binding domain. Activation of the CaR, descriptions of CaRs isolated from different sources, and examples of CaR active compound are provided

in Nemeth *NIPS 10*:1-5, 1995, Brown *et al.* U.S. Patent No. 5,688,938, Van Wagenen *et al.*, International Application Number PCT/US97/05558 International Publication Number WO 97/37967, Brown E.M. et al., *Nature* 366:575, 1993, Riccardi D., et al., *Proc. Nat'l. Acad. Sci. USA* 92:131-135, 1995, and Garrett J.E., et al., *J. Biol. Chem.* 31:12919-12925, 1995. (Each of these references are hereby incorporated by reference herein.) Brown *et al.* U.S. Patent No. 5,688,938 and Van Wagenen *et al.*, International Application Number PCT/US97/05558 International Publication Number WO 97/37967, describe different types of compounds active at the CaR including compounds which appear to be allosteric modulators and CaR antagonists.

The CaR can be targeted to achieve therapeutic effects. Examples of target diseases are provided in Brown *et al.* U.S. Patent No. 5,688,938, and Van Wagenen *et al.*, International Application Number PCT/US97/05558 International Publication Number WO 97/37967, and include hyperparathyroidism and osteoporosis.

γ-Aminobutyric acid Receptors ($GABA_BRs$)

$GABA_BRs$ are G-protein coupled metabotropic receptors. $GABA_BRs$ modulate synaptic transmission by inhibiting presynaptic transmitter release and by increasing K^+ conductance responsible for long-lasting inhibitory postsynaptic potentials. (*See,* Kaupmann *et al., Nature 386*:239-246, 1997, hereby incorporated by reference herein.)

$GABA_BRs$ are found in the mammalian brain, in locations outside of the brain, and in lower species. Outside of the brain, $GABA_BRs$ have been identified on axon terminals and ganglion cell bodies of the autonomic nervous system, on fallopian tube and uterine intestinal smooth muscle cells, in the kidney cortex, urinary bladder muscle and on testicular interstitial cells. (*See,* Bowery, *Annu. Rev. Pharmacol. Toxicol. 33*:109-147, 1993, hereby incorporated by reference herein.)

Different $GABA_BRs$ subtypes exist. Kaupmann *et al., Nature 386*:239-246, 1997, indicate that they cloned $GABA_BRs$. Nucleic acid encoding two $GABA_BR$ proteins were indicated to be cloned from rat brain: $GABA_BR1a$ and $GABA_BR1b$. $GABA_BR1a$ differs from $GABA_BR1b$ in that the N-terminal 147 residues are replaced by 18 amino acids. $GABA_BR1a$ and $GABA_BR1b$ appear to be splice variants. The cloned $GABA_BRs$ were indicated to negatively couple adenylyl cyclases and show sequence similarity to the metabotropic receptors for L-glutamate (mGluR). Northern blot analysis indicated that

GABA$_B$R1a and GABA$_B$R1b is present in brain and testis, but not in kidney, skeletal muscle, liver, lung, spleen, or heart.

Kaupmann *et al.,* International Application Number PCT/EP97/01370, International Publication Number WO 97/46675, indicate that they have obtained rat GABA$_B$R clones, GABA$_B$R1a and GABA$_B$R1b; and humans GABA$_B$R clones, GABA$_B$R1a/b (representing a partial receptor clone) and GABA$_B$R1b (representing a full-length receptor clone). Amino acid sequence information, and encoding cDNA sequence information, is provided for the different GABA$_B$R clones.

Another GABA$_B$R subtype is GABA$_B$R2. Northern blot analysis reveals than an approximately 6.3 Kb human GABA$_B$R2 transcript is abundantly expressed in the human brain. Expression is not detected in the heart, placenta, lung, liver, skeletal muscle, kidney and pancreas under conditions where GABA$_B$R2 transcript was identified in the human brain. Within the human brain GABA$_B$R2 is broadly expressed at variable levels.

GABA$_B$R functions as a heterodimer of the subunits GABA$_B$R1 or GABA$_B$R2. (Jones *et al. Nature 396*:674-679, 1998, hereby incorporated by reference herein.)

GABA$_B$Rs have been targeted to achieve therapeutic effects. Kerr and Ong, DDT 1:371-380, 1996, describe different compounds indicated to be GABA$_B$R agonists and GABA$_B$R antagonists. Kerr and Ong also review therapeutic implications of affecting GABA$_B$R activity including, spasticity and motor control, analgesia, epilepsy, cognitive effects, psychiatric disorders, alcohol dependence and withdrawal, feeding behavior, cardiovascular and respiratory functions, and peripheral functions.

Bittiger *et al., Tips 4*:391-394, 1993, review therapeutic applications of GABA$_B$R antagonists. Potential therapeutic applications noted by Bittiger *et al.* include cognitive processes, epilepsy, and depression.

G-Protein Fusion Receptors

Examples of some different types of G-protein fusion receptors, and advantages of some receptors, are provided below. Using the present application as guide additional G-protein receptors fusion can be constructed.

G-protein fusion receptors contain an intracellular domain of a receptor fused to a G-protein subunit (G). G fusions to adrenoreceptors have been reported by Bertin *et al., Receptors and Channels 5*:41-51, 1997; Wise and Milligan, *Journal of Biological Chemistry 39*:24673-24678, 1997; and Bertin *et al., Proc. Natl. Acad. Sci. USA 91*:8827-

8831, 1994 (each of which are hereby incorporated by reference herein). These studies were indicated to produce a functional chimeric by fusing the $_{2A}$-adrenoreceptor to the G_{i1} , or the $_{2}$-adrenoreceptor to the G_{s} .

The G-protein fusion receptors described by the present invention include a G-protein fused to an intracellular domain, where the intracellular domain when present in a wild type receptor does not interact with that type of G-protein. Thus, the present invention also describes swapping of signals by fusing an intracellular domain to a G normally not coupled to that intracellular domain. The use of such fusion proteins, while applicable to chimeric $GABA_BRs$, is not limited to chimeric $GABA_BRs$. Indeed, such technology can be applied to receptors containing an extracellular domain, transmembrane domain and intracellular domain of a wild type receptor.

Preferred G-proteins fusion receptors contain an intracellular domain fused to a promiscuous G that couples to phospholipase C resulting in the mobilization of intracellular calcium. Increases in intracellular calcium can be conveniently measured through the use of dyes. Such techniques are well known in the art and are described, for example by Brown *et al.* U.S. Patent No. 5,688,938.

In an embodiment G-proteins fusions can also be used to decrease receptor desensitization.

Examples of promiscuous G 's coupling to phospholipase C include naturally occurring G-proteins such as G_{15} and G_{16}, and chimeric G-protein such as Gqo5 and Gqi5. Gqo5 and Gqi5 are made of a Gq portion where the five amino acids at the C-terminal are from either G_o or G_i, respectively (Conklin *et al., Nature 363*:274-277, 1993, hereby incorporated by reference herein). The Gq portion of such chimeric receptors provides for phospholipase C coupling while the terminal G_o or G_i portion allows the chimeric G-protein to couple to different receptor proteins that are normally involved in inhibitor effects on adenylate cyclase.

In an embodiment of the present invention the employed G-protein is from a human source or is made up of different G-protein components each from a human source.

G-proteins fusions can be created, for example, by fusing directly or indirectly the intracellular domain of a receptor protein to a polypeptide having an amino acid sequence substantially similar to G_{15}, G_{16}, Gqo5 or Gqi5. In different embodiments, the receptor

is fused directly or indirectly to a G-protein consisting of the amino acid sequence of G $_{15}$, G $_{16}$, Gqo5 or Gqi5.

The intracellular domain portion of a receptor protein fused directly or indirectly to a G-protein should be at least about 1 amino acid in length. In different embodiments the portion is at least about 10 amino acids, is at least about 50 amino acids, at least about 100 amino acids, or the full length of an intracellular domain.

The intracellular domain can be directly linked to a G-protein or can be indirectly linked through an optionally present linker. Optionally present linkers are preferably about 3 to about 30 amino acids in length. Preferred linkers are made up of alanine, glycine, or a combination thereof.

Chimeric Receptors

Examples of some different types of chimeric receptors, and advantages of some receptors, are provided below. Using the present application as guide additional chimeric receptors can be constructed.

Chimeric GABA$_B$R Extracellular Domain

Chimeric GABA$_B$Rs containing a GABA$_B$R extracellular domain are particularly useful for studying the importance of the GABA$_B$R extracellular domain and assaying for compounds active at the extracellular domain. Preferably chimeric GABA$_B$Rs containing a GABA$_B$R extracellular domain also contain a CaR intracellular domain.

A variety of different activities have been generally attributed to GABA$_B$R subtypes. (*E.g.*, Kerr and Ong, DDT 1:371-380, 1996.) Kaupmann *et al.*, *Nature 386*:239-246, 1997, report that in preliminary experiments involving GABA$_B$R1a they did not detect positive coupling to the adenylyl cyclase or coupling to the phospholipase effector system.

An intracellular CaR domain can be used to couple with G-proteins which activate phospholipase C and mobilize intracellular calcium. Mobilization of intracellular calcium is readily detected, for example, by fluorescent indicators of intracellular Ca^{2+}.

An additional advantage of using the intracellular CaR domain is that CaR G-protein activation is not rapidly desensitized. Thus, the intracellular CaR domain can be used to produce a stronger intracellular signal than a signal produced from a receptor which is desensitized rapidity.

More preferably, the chimeric $GABA_BR$ contains an intracellular CaR domain, and also contains either a CaR or a $GABA_BR$ transmembrane domain. Advantages of using a CaR transmembrane domain include separating the effects occurring at a $GABA_BR$ extracellular domain from effects occurring at a transmembrane domain; and providing additional intracellular elements, present on transmembrane intracellular loops, useful for coupling to G-protein.

A $GABA_BR$ transmembrane domain is useful for examining whether the transmembrane $GABA_BR$ can be targeted to affect $GABA_BR$ activity, and obtaining compounds active at the $GABA_BR$ transmembrane domain. For example, a transmembrane $GABA_BR$ can be used to screen for transmembrane allosteric modulators and antagonists.

Chimeric $GABA_BR$ Transmembrane Domain

Chimeric $GABA_BRs$ containing a $GABA_BR$ transmembrane are particularly useful for studying the importance of the $GABA_BR$ transmembrane domain and assaying for compounds active at the transmembrane domain. Preferably Chimeric $GABA_BRs$ containing a $GABA_BR$ transmembrane domain contain an extracellular domain which is either mGluR8 or CaR, and an intracellular CaR domain.

More preferably, the chimeric $GABA_BR$ contains an extracellular domain from either mGluR8 or CaR, a $GABA_BR$ transmembrane, and an intracellular CaR domain. A chimeric $GABA_BR$ containing extracellular mGluR8 or CaR domains can readily be stimulated using mGluR8 or CaR ligands.

Chimeric $GABA_BR$ Intracellular Domain

Chimeric $GABA_BRs$ containing a $GABA_BR$ intracellular domain are particularly useful for studying the importance of the $GABA_BR$ intracellular domain and assaying for compounds active at the intracellular domain. Preferably, the chimeric receptors contain an extracellular domain from either mGluR8 or CaR. The extracellular mGluR8 or CaR domains can readily be activated using mGluR8 or CaR ligands.

Receptor Domains

Domains of a G-protein fusion receptor, a chimeric receptor, and G , substantially similar to a particular sequence can be readily produced using the disclosure provided

herein in conjunction with information well known in the art. Substantially similar sequences can be obtained taking into account sequence information for a particular type of receptor obtained from different sources, different types of amino acids which are to some extent interchangeable, and the ease of experimentation with which functional receptor activity can be assayed.

Substantially similar sequences includes amino acid alterations such as deletions, substitutions, additions, and amino acid modifications. A "deletion" refers to the absence of one or more amino acid residue(s) in the related polypeptide. An "addition" refers to the presence of one or more amino acid residue(s) in the related polypeptide. Additions and deletions to a polypeptide may be at the amino terminus, the carboxy terminus, and/or internal. Amino acid "modification" refers to the alteration of a naturally occurring amino acid to produce a non-naturally occurring amino acid. A "substitution" refers to the replacement of one or more amino acid residue(s) by another amino acid residue(s) in the polypeptide. Derivatives can contain different combinations of alterations including more than one alteration and different types of alterations.

The sequences of polypeptides can be compared from different sources to help identify variable amino acids not essential for receptor activity. For example, Figure 7 provides the rat $GABA_BR1a$ and $GABA_BR1b$ amino acid sequences. The rat $GABA_BR1a$ and $GABA_BR1b$ amino acid sequences can be compared with the human $GABA_BR1a$ and $GABA_BR1b$ sequences to identify conserved and variable amino acids. Derivatives can then be produced where a variable amino acid is changed, and receptor activity can be readily tested.

Similarly, the amino acid sequences for CaR, mGluR8, and G-proteins from different sources are either known in the art or can readily be obtained. Examples of such references are provided above.

While the effect of an amino acid change varies depending upon factors such as phosphorylation, glycosylation, intra-chain linkages, tertiary structure, and the role of the amino acid in the active site or a possible allosteric site, it is generally preferred that a substituted amino acid is from the same group as the amino acid being replaced. To some extent the following groups contain amino acids which are interchangeable: the basic amino acids lysine, arginine, and histidine; the acidic amino acids aspartic and glutamic acids; the neutral polar amino acids serine, threonine, cysteine, glutamine, asparagine and, to a lesser extent, methionine; the nonpolar aliphatic amino acids glycine, alanine, valine,

isoleucine, and leucine (however, because of size, glycine and alanine are more closely related and valine, isoleucine and leucine are more closely related); and the aromatic amino acids phenylalanine, tryptophan, and tyrosine. In addition, although classified in different categories, alanine, glycine, and serine seem to be interchangeable to some extent, and cysteine additionally fits into this group, or may be classified with the polar neutral amino acids.

While proline is a nonpolar neutral amino acid, its replacement represents difficulties because of its effects on conformation. Thus, substitutions by or for proline are not preferred, except when the same or similar conformational results can be obtained. The conformation conferring properties of proline residues may be obtained if one or more of these is substituted by hydroxyproline (Hyp).

Examples of modified amino acids include the following: altered neutral nonpolar amino acids such as -amino acids of the formula $H_2N(CH_2)_nCOOH$ where n is 2-6, sarcosine (Sar), tbutylalanine (t-BuAla), t-butylglycine (t-BuGly), N-methyl isoleucine (N-MeIle), and norleucine (Nleu); altered neutral aromatic amino acids such as phenylglycine; altered polar, but neutral amino acids such as citrulline (Cit) and methionine sulfoxide (MSO); altered neutral and nonpolar amino acids such as cyclohexyl alanine (Cha); altered acidic amino acids such as cysteic acid (Cya); and altered basic amino acids such as ornithine (Orn).

Preferred derivatives have one or more amino acid alteration(s) which do not significantly affect the receptor activity of the related receptor protein. In regions of receptor domains not necessary for receptor activity, amino acids may be deleted, added or substituted with less risk of affecting activity. In regions required for receptor activity, amino acid alterations are less preferred as there is a greater risk of affecting receptor activity.

Derivatives can be produced using standard chemical techniques and recombinant nucleic acid techniques. Modifications to a specific polypeptide may be deliberate, as through site-directed mutagenesis and amino acid substitution during solid-phase synthesis, or may be accidental such as through mutations in hosts which produce the polypeptide. Polypeptides including derivatives can be obtained using standard techniques such as those described by Sambrook *et al., Molecular Cloning,* Cold Spring Harbor Laboratory Press (1989). For example, Chapter 15 of Sambrook describes procedures for site-directed mutagenesis of cloned DNA.

Receptor Nucleic Acid

G-protein fusion and chimeric receptor nucleic acid can be produced based on the information provided herein along with standard recombinant nucleic acid techniques. Examples of references describing recombinant nucleic acid techniques include *Molecular Cloning*, Sambrook *et al.,* Cold Spring Harbor Laboratory Press (1989); and *Current Protocols in Molecular Biology,* Frederick *et al.*, John Wiley & Sons, Inc. (1995).

Due to the degeneracy of the genetic code different nucleic acid sequences can encode for a particular polypeptide. Thus, a large number of nucleic acids encoding for a receptor having the same amino acid sequence can be produced.

An embodiment of the present invention uses human nucleic acid encoding for the domains from CaR, $GABA_BR1A$, $GABA_BR1B$, $GABA_BR2$ and/or mGluR8. The amino acid sequences of different domains is provided in Figures 1-3.

Recombinant Cells

Nucleic acid expressing a functional G-Protein fusion or a chimeric receptor can be used to create transfected cells lines expressing such receptors. Such cell lines have a variety of uses such as being used for high-throughput screening for compounds modulating receptor activity; being used to assay binding to the receptor; and as factories to produce large amounts of a receptor.

A variety of cell lines can couple exogenously expressed receptors to endogenous functional responses. Cell lines such as NIH-3T3, HeLa, NG115, CHO, HEK 293 and COS7 which are expected to lack CaR, mGluR8, and $GABA_BR$ can be tested to confirm that they lack these receptors.

Production of stable transfectants can be accomplished by transfection of an appropriate cell line with, for example, an expression vector such as pMSG vector, in which the coding sequence for the G-protein fusion or chimeric $GABA_BR$ cDNA has been cloned. Expression vectors containing a promoter region, such as the mouse mammary tumor virus promoter (MMTV), drive high-level transcription of cDNAs in a variety of mammalian cells. In addition, these vectors contain genes for selecting cells stably expressing cDNA of interest. The selectable marker in the pMSG vectors encode an

enzyme, xanthine-guanine phosphoribosyl transferase (XGPRT), conferring resistance to a metabolic inhibitor that is added to the culture to kill nontransfected cells.

The most effective method for transfection of eukaryotic cell lines with plasmid DNA varies with the given cell type. The expression construct will be introduced into cultured cells by the appropriate technique, such as Ca^{2+} phosphate precipitation, DEAE-dextran transfection, lipofection or electroporation. Expression of the receptor cDNA in cell lines can be assessed by solution hybridization and Northern blot analysis.

Binding Assays

The present invention also includes using G-protein fusion receptors or chimeric $GABA_BR$ in a binding assay. G-protein fusion receptors or chimeric $GABA_BRs$ having a particular $GABA_BR$ domain can be used, for example to facilitate obtaining compounds able to bind to that particular receptor domain; and to determine whether a compound which binds to a particular domain. For example, in a complete chimeric $GABA_BR$ containing extracellular, transmembrane, and intracellular domains, the presence of one or more domains from CaR or mGluR are useful to present $GABA_BR$ domain(s) to a binding agent in a form more like the $GABA_BR$ domain(s) in the wild type receptor compared to an incomplete $GABA_BR$ receptor fragment lacking one or more domains.

Binding assays can be carried out using techniques well known in the art. Binding assays preferably employ radiolabeled binding agents.

An example of a binding procedure is carried out by first attaching chimeric $GABA_BR$ to a solid-phase support to create an affinity matrix. The affinity matrix is then contacted with potential $GABA_BR$ binding agents. A large library of compounds may be used to determine those compounds binding to the affinity matrix. Bound compounds can be eluted from the column.

Therapeutic Modulation

As pointed out above, different types of diseases and disorders can be treated using compounds modulating CaR, mGluR, or $GABA_BR$ activity. Additionally, such compounds can be used prophylactically. Compounds modulating $GABA_BR2$ activity can be administered to patients who would benefit from such treatment. Patients are mammals, preferably humans.

Modulators of CaR, mGluR, or $GABA_BR$ activity can be administered to a patient using standard techniques. Techniques and formulations generally may be found in Remington's Pharmaceutical Sciences, 18th ed., Mack Publishing Co., Easton, PA, 1990 (hereby incorporated by reference herein).

Suitable dosage forms, in part, depend upon the use or the route of entry, for example, oral, transdermal, transmucosal, or by injection (parenteral). Such dosage forms should allow the therapeutic agent to reach a target cell whether the target cell is present in a multicellular host or in culture. For example, pharmacological compounds or compositions injected into the blood stream should be soluble. Other factors are well known in the art, and include considerations such as toxicity and dosage forms which retard the therapeutic agent from exerting its effect.

Therapeutic compounds can be formulated as pharmaceutically acceptable salts and complexes thereof. Pharmaceutically acceptable salts are non-toxic salts in the amounts and concentrations at which they are administered. The preparation of such salts can facilitate the pharmacological use by altering the physical characteristics of the compound without preventing it from exerting its physiological effect. Useful alterations in physical properties include lowering the melting point to facilitate transmucosal administration and increasing the solubility to facilitate administering higher concentrations of the drug.

The pharmaceutically acceptable salt of a compound may be present as a complex. Examples of complexes include an 8-chlorotheophylline complex (analogous to, *e.g.*, dimenhydrinate:diphenhydramine 8-chlorotheophylline (1:1) complex; Dramamine) and various cyclodextrin inclusion complexes.

Pharmaceutically acceptable salts include acid addition salts such as those containing sulfate, hydrochloride, fumarate, maleate, phosphate, sulfamate, acetate, citrate, lactate, tartrate, methanesulfonate, ethanesulfonate, benzenesulfonate, *p*-toluene-sulfonate, cyclohexylsulfamate and quinate.

Pharmaceutically acceptable salts can be obtained from acids such as hydrochloric acid, maleic acid, sulfuric acid, phosphoric acid, sulfamic acid, acetic acid, citric acid, lactic acid, tartaric acid, malonic acid, methanesulfonic acid, ethanesulfonic acid, benzenesulfonic acid, *p*-toluenesulfonic acid, cyclohexylsulfamic acid, fumaric acid, and quinic acid.

Pharmaceutically acceptable salts also include basic addition salts such as those containing benzathine, chloroprocaine, choline, diethanolamine, ethylenediamine, meglumine, procaine, aluminum, calcium, lithium, magnesium, potassium, sodium, ammonium, alkylamine, and zinc, when acidic functional groups, such as carboxylic acid or phenol are present. For example, see Remington's Pharmaceutical Sciences, 18th ed., Mack Publishing Co., Easton, PA, p. 1445, 1990. Such salts can be prepared using the appropriate corresponding bases.

Carriers or excipients can also be used to facilitate administration of therapeutic agents. Examples of carriers include calcium carbonate, calcium phosphate, various sugars such as lactose, glucose, or sucrose, or types of starch, cellulose derivatives, gelatin, vegetable oils, polyethylene glycols and physiologically compatible solvents. Examples of physiologically compatible solvents include sterile solutions of water for injection (WFI), saline solution and dextrose.

$GABA_BR$ modulating compounds can be administered by different routes including intravenous, intraperitoneal, subcutaneous, intramuscular, oral, topical (transdermal), or transmucosal administration. For systemic administration, oral administration is preferred. For oral administration, for example, the compounds can be formulated into conventional oral dosage forms such as capsules, tablets, and liquid preparations such as syrups, elixirs, and concentrated drops.

Alternatively, injection (parenteral administration) may be used, *e.g.*, intramuscular, intravenous, intraperitoneal, and subcutaneous. For injection, compounds are formulated in liquid solutions, preferably, in physiologically compatible buffers or solutions, such as saline solution, Hank's solution, or Ringer's solution. In addition, the compounds may be formulated in solid form and redissolved or suspended immediately prior to use. Lyophilized forms can also be produced.

Systemic administration can be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are well known in the art, and include, for example, for transmucosal administration, bile salts and fusidic acid derivatives. In addition, detergents may be used to facilitate permeation. Transmucosal administration, for example, may be through nasal sprays, rectal suppositories, or vaginal suppositories.

For topical administration, compounds can be formulated into ointments, salves, gels, or creams, as is well known in the art.

The amounts of various $GABA_BR$ modulating compounds to be administered can be determined by standard procedures taking into account factors such as the compound IC_{50}, EC_{50}, the biological half-life of the compound, the age, size and weight of the patient, and the disease or disorder associated with the patient. The importance of these and other factors to be considered are well known to those of ordinary skill in the art. Generally, the amount is expected to preferably be between about 0.01 and 50 mg/kg of the animal to be treated.

EXAMPLES

Examples are provided below illustrating different aspects and embodiments of the present invention. The examples include techniques that can be used to produce and use G-protein fusion receptors and chimeric receptors. These examples are not intended to limit the claimed invention.

Example 1: Construction of G-Protein Fusions

This example illustrates different G-protein fusion receptor_constructs and techniques used to produce different G-protein fusion receptor constructs. Numbering of nucleotide position for all the following constructs is such that nucleotide number 1 corresponds to the A of the ATG start codon of the nucleotide sequence encoding the designated protein.

I. FULL-LENGTH CONSTRUCTS

A. phCaR

The cDNA encoding the human CaR (Garrett et al., (1995) J. Biol. Chem.270:12919) is harbored in the Bluescript SK(-) plasmid (Stratagene). This construct is referred to as phCaR.

B. phmGluR2

A full length human mGluR2 cDNA was amplified from human cerebellum MarathonReady cDNA (Clontech) using PCR primers based on the human mGluR2 cDNA sequence (Genbank Accession # 4504136). The obtained PCR fragment was

subcloned into the pT7Blue TA vector (Novagen). A Hind III-Not I fragment containing the human mGluR2 cDNA was then subcloned into the Bluescript SKII(-) plasmid (Stratagene). This construct is referred to as phmGluR2.

C. phGα_q

A full length human Gα_q cDNA was amplified from human cerebral cortex Quick-Clone cDNA (Clontech) using PCR primers based on the human Gα_q cDNA sequence (Genbank Accession # 4504044). The obtained PCR fragment was subcloned into the Bluescript SKII(-) plasmid (Stratagene). This construct is referred to as phGα_q.

D. phmGluR8

The cDNA encoding the full length human mGluR8 cDNA (Stormann *et al.,* U.S. Patent Nos. 6,051,688, 6,077,675, and 6,084,084) is harbored in the Bluescript SKII(-) plasmid (Stratagene). This construct is referred to as phmGluR8.

E. ph8SPmGluR4

A full length human mGluR4 cDNA was amplified from human cerebellum MarathonReady cDNA (Clontech) using PCR primers based on the human mGluR4 cDNA sequence (Genbank Accession #X80818). The obtained PCR fragment was cloned into the pT7Blue TA vector (Novagen). A 2977 bp BamHI fragment containing the human mGluR4 cDNA was then subcloned into the vector pcDNA3.1/Hygro+ (Invitrogen). This construct is referred to as phmGluR4.

Next, the predicted signal peptide of mGluR4 was replaced with the predicted signal peptide and 87 bp of 5' UTR from phmGluR8 using a recombinant PCR strategy similar to those described above. The first reaction used a phmGluR8 construct with two primers, 3.1-535F (sense 21-mer, complementary to vector sequence upstream of the hmGluR8 insert; sequence 5'-ggcattatgcccagtacatga-3'), and the hybrid primer 8/4RP (antisense 42-mer, containing 21 nucleotides complementary to human mGluR8 and 21 nucleotides complementary human mGluR4; sequence 5'-caagcctctcttcccaggcattttctccacaggtggtattgc-3'). These primers were used to amplify a 469 bp PCR fragment of human mGluR8.

In a separate PCR reaction using phmGluR4 as template, a 472 bp fragment of

human mGluR4 was amplified using a hybrid primer 4/8RP (sense 42-mer, exactly complementary to primer 8/4RP) and oligo mG4-472R, (antisense 18-mer, complementary to the human mGluR4 cDNA; sequence 5'-ctgaagcaccgatgacac-3'). The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers mG4-472R and 3.1-535F, and Turbo Pfu DNA polymerase (Stratagene).

The resulting chimeric PCR product was digested with NarI and NheI (New England Biolabs) and subcloned into phmGluR4 digested with the same two restriction enzymes. The sequence of the resultant chimeric construct, ph8SPmGluR4, was verified by ABI automated DNA sequence analysis.

The replacement of the predicted signal peptide of mGluR4 with that of mGluR8 greatly increased the activity of this receptor in *in vitro* assays

II. $G\alpha_q i5$

The cDNA encoding the human $G\alpha_q i5$ cDNA (Conklin et al (1993) Nature 363:274-77) is harbored in the Bluescript SKII(-) plasmid (Stratagene). This construct is referred to as $G\alpha_q i5$. The nucleic acid and amino acid sequences for $G\alpha_q i5$ are provided by SEQ. ID. NOs. 28 and 29 respectively.

III. phCaR/hmGluR2

This chimera contains the extracellular domain of the human CaR and transmembrane domain and intracellular cytoplasmic tail of human mGluR2. The chimeric junction between the CaR and hmGluR2 was created using a recombinant PCR strategy similar to those described above.

The first reaction used two primers, CA1156 (sense 19-mer, corresponding to nucleotides 1156-1174 of human CaR), and the hybrid primer CA/2 (antisense 42-mer, containing 21 nucleotides complementary to nucleotides 1774-1794 of human CaR and 21 nucleotides complementary to nucleotides 1660-1680 of the human mGluR2). These primers were used to amplify a 659 bp PCR fragment of human CaR.

In a separate PCR reaction using phmGluR2 as template, a 692 bp fragment of the human mGluR2 was amplified using a hybrid primer 2/CA (sense 42-mer, exactly complementary to primer CA/2) and oligo 2-2330m, (antisense 23-mer, complementary to

nucleotides 2309-2331 of the human mGluR2 cDNA). The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers CA1156 and 2-2330m, and the Pfu DNA polymerase (Stratagene).

The resulting chimeric PCR product was digested with SexA1 (Boehringer Mannheim) and BamHI (New England Biolabs) and subcloned into phCaR digested with the same two restriction enzymes. In the final cloning step, the 3' end of human mGluR2 was subcloned into this construct using the restriction enzymes BsrGI and BamHI (both New England Biolabs). The sequence of the resultant chimeric construct, phCaR/hmGluR2, was verified by ABI automated DNA sequence analysis.

IV. phCaR/hmGluR2*Gqi5

This construct contains the phCaR/hmGluR2 chimeric receptor fused to human $G\alpha_q i5$. A HindIII-BamHI fragment containing the phCaR/hmGluR2 construct was subcloned into pcDNA3.1/Hygro(+) (Invitrogen) to aid in constructing this fusion protein. The chimeric junction between the C-terminus of phCaR/hmGluR2 and the N-terminus of $G\alpha_q i5$ was created using a recombinant PCR strategy similar to those described above.

The first reaction used two primers, 2-1713 (sense 21-mer, corresponding to nucleotides 1710-1730 of human mGluR2) and the hybrid primer 2/Q (antisense 42-mer, containing 21 nucleotides complementary to nucleotides 2596-2616 of human mGluR2, and 21 nucleotides complementary to nucleotides 1-21 of $pG\alpha_q i5$). These primers were used to amplify a 927 bp PCR fragment of phCaR/hmGluR2. In a separate PCR reaction all of $G\alpha_q i5$ was amplified using a hybrid primer Q/2 (sense 42-mer, exactly complementary to primer 2/Q) and the and the T3 primer commercially available from Stratagene.

These two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers 2-1713 and T3, and the Pfu DNA polymerase (Stratagene). The resulting chimeric PCR product was digested with Bsu361 and BamHI (New England Biolabs) and subcloned into phCaR/hmGluR2 digested with the same two restriction enzymes. The sequence of the resultant chimeric fusion construct, phCaR/hmGluR2*$G\alpha_q i5$, was verified by DNA sequence analysis.

V. phmGluR2//CaR Construct

This chimera contains the extracellular and transmembrane domains of human mGluR2 linked to the intracellular cytoplasmic tail domain of the human CaR. The chimeric junction was created using three separate PCR reactions.

The first reaction used two primers, 2-1713 (sense 21-mer, corresponding to nucleotides 1710-1730 of human mGluR2, Genbank Accession # 4504136) and the hybrid primer 2/CT (antisense 42-mer, containing 21 nucleotides complementary to nucleotides 2452 – 2472 of human mGluR2 and 21 nucleotides complementary to nucleotides 2602-2622 of the human CaR). These primers were used to amplify a 783 bp PCR fragment of human mGluR2. In a separate PCR reaction using phCaR in the BlueScript SK$^-$ plasmid as template, a 750 bp fragment of the human CaR was amplified using a hybrid primer CT/2 (sense 42-mer, exactly complementary to primer 2/CT) and the T3 primer commercially available from Stratagene.

The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers 2-1713 and T3, and the Pfu DNA polymerase (Stratagene). The resulting chimeric PCR product was digested with BsrG I and Not I (New England Biolabs) and subcloned into pmGluR2 digested with the same two restriction enzymes. The sequence of the resultant chimeric construct, pmGluR2//CaR, was verified by ABI automated DNA sequence analysis.

VI. pmGluR2//CaR*Gα_qi5 Construct

This construct contains the hmGluR2//CaR chimeric receptor fused to human Gα_qi5. The chimeric junction between the C-terminus of hmGluR2//CaR and the N-terminus of Gα_qi5 was created using a recombinant PCR strategy similar to that described above for the construction of phmGluR2//CaR.

The first reaction used two primers, CRP10A (sense 18-mer, corresponding to nucleotides 2812-2829 of phCaR) and the hybrid primer CaRQ (antisense 42-mer, containing 21 nucleotides complementary to nucleotides 3214– 3234 phCaR, and 21 nucleotides complementary to nucleotides 1-21 of pGα_qi5). These primers were used to amplify a 443 bp PCR fragment of hmGluR2//CaR. In a separate PCR reaction, all of Gα_qi5 was amplified using a hybrid primer QCaR (sense 42-mer, exactly complementary

to primer CaRQ) and the T3 primer commercially available from Stratagene.

The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers CRP10A and T3, and the Pfu DNA polymerase (Stratagene). The resulting chimeric PCR product was digested with BstE II and Not I (New England Biolabs) and subcloned into pmGluR2//CaR digested with the same two restriction enzymes. The sequence of the resultant chimeric fusion construct, pmGluR2//CaR*Gα_qi5, was verified by ABI automated DNA sequence analysis.

VII. Fusion Receptor Protein Linker Addition Constructs

A. phmGluR2//CaR*AAA*Gα_qi5

A linker encoding three alanine residues was incorporated into the phmGluR2//CaR*Gα_qi5 construct by mutagenesis (Stratagene QuickChange Mutagenesis Kit). A sense 40-mer, 2CQ+LP, contained 16 nucleotides corresponding to 3219-3234 of human CaR, followed by the 9 nucleotide sequence (GCGGCCGCC) encoding three alanine residues and a NotI restriction enzyme site, and then 15 nucleotides corresponding to nucleotides 1-15 of Gα_qi5. 2CQ+LP was annealed to an antisense 40-mer, 2CQ+LM, the exact complement of 2CQ+LP. These oligos were used in the mutagenesis reaction according to the manufacturer's protocol. Restriction enzyme analysis and DNA sequence analysis confirmed the insertion of the 9 nucleotide linker (GCGGCCGCC) between the C-terminus of phmGluR2//CaR and the N-terminus of Gα_qi5. This construct was designated phmGluR2//CaR*AAA*Gα_qi5.

B. Human GABA$_B$R2*AAA*Gα_qo5 and human GABA$_B$R1a*AAA*Gα_qo5

These constructs contain the human GABA$_B$R2 (hGABA$_B$R2: Genbank Accession # AJ 012188) and human GABA$_B$R1a (hGABA$_B$R1a: Genbank Accession # AJ 012185) fused at their C-terminus to the N-terminus of human Gα_qo5 (hGα_qo5: *Nature* 363:274-276, 1993). Human GABA$_B$R2, hGABA$_B$R1a, and hGα_qo5 were cloned into the plasmid pcDNA3.1/Hygro+ (Invitrogen) and are designated phGABA$_B$R2, phGABA$_B$R1a, and phGα_qo5. The first reaction used two primers, XcmI-R2 (sense 20-mer, corresponding to nucleotides 2650-2669 of phGABA$_B$R2) and the hybrid primer R2/Go5(-) (antisense 45-

mer, containing 18 nucleotides complementary to nucleotides 2806-2823 of phGABA$_B$R2 and 18 nucleotides complementary to nucleotides 1-18 of hGα_qo5). These two complementary areas flank a 9 nucleotide sequence coding for 3 alanine sequences with a unique NotI restriction site. These primers were used to amplify a 200 base-pair PCR fragment.

In a separate PCR reaction, part of hGα_qo5 was amplified using a hybrid primer R2/Gα_qo5(+) (sense 45-mer), exactly complementary to R2/Go5(-) and XbaI-Go5 primer (22-mer containing 22 nucleotides complementary to nucleotides 873-895 of hGα_qo5) These primers were used to amplify a 914 base-pair PCR product. The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers; XcmI-R2 and XbaI-Go5, and Pfu polymerase (Stratagene).

The resulting chimeric PCR product was digested with the restriction endonucleases XcmI and XbaI (New England Biolabs) and subcloned into phGABA$_B$R2 digested with the same two restriction enzymes. The resulting clone was then digested with HindIII and XbaI and subcloned into phGα_qo5 cut with HindIII and XbaI resulting in the chimeric hGABA$_B$R*AAA*Gα_qo5. The chimeric junction between the C-terminus hGABA$_B$R1a, the Ala linker, and the N-terminus of hGα_qo5 was created using a recombinant PCR strategy similar to those described above.

To construct hGABA$_B$R1a*AAA*Gqo5, the first reaction used a commercially available T7 primer (Novagen) and the NtI hGBR1 primer (CAGAGTCATGGCGGCCGCCTTATAAAGCAAATGCACTCG) corresponding to nucleotide numbers 1-9 of hGα_qo5 and nucleotide numbers 2863-2883 of hGABA$_B$R1a.

C. <u>phmGluR8//CaR*AAA*Gα_qi5</u>

A linker encoding three alanine residues was incorporated into the phmGluR8//CaR*Gα_qi5 construct by mutagenesis (Stratagene QuickChange Mutagenesis Kit), exactly as described in Section A, above to create phmGluR2//CaR*AAA*Gα_qi5. The same primers, 2CQ+LP and 2CQ+LM, were used for this mutagenesis. Restriction enzyme analysis and DNA sequence analysis confirmed the insertion of the 9-nucleotide linker (GCGGCCGCC) between the C-terminus of phmGluR8//CaR and the N-terminus of Gα_qi5. This construct was designated phmGluR8//CaR*AAA*Gα_qi5.

D. ph8SPmGluR4//CaR*AAA*Gα_qi5

This chimera contains the extracellular and transmembrane domains of the human 8SPmGluR4 construct and intracellular cytoplasmic tail of human CaR fused to Gα_qi5 through the three alanine residue linker.

The chimeric junction between the human 8SPmGluR4 and hCaR was created using a recombinant PCR strategy similar to those previously described. The first reaction used two primers, mG4-2028R (sense 19-mer, corresponding to nucleotides of human 8SPmGluR4; sequence5'-catctaccgcatcttcgag-3'), and the hybrid primer 4CT (antisense 42-mer, containing 21 nucleotides complementary to human 8SPmGluR4 and 21 nucleotides complementary human CaR; sequence 5'-acgcacctcctcgatggtgttctgctccgggtggaagaggat –3'). These primers were used to amplify a 549 bp PCR fragment from human 8SPmGluR4.

In a separate PCR reaction, using phmGluR2//CaR*AAA*Gα_qi5 as a template, a 743 bp fragment of the human CaR*AAA*Gα_qi5 was amplified using the hybrid primer CT4 (sense 42-mer, exactly complementary to primer 4CT) and oligo Gaqi58R, (antisense 21-mer, complementary to Gα_qi5 cDNA; sequence 5'- ctcgatctcgtcgttgatccg -3'). The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers mG4-2028R and Gaqi58R, and Pfu DNA polymerase (Stratagene).

The resulting chimeric PCR product was digested sequentially with KpnI and NotI (New England Biolabs) and subcloned into ph8SPmGluR4 prepared with the same two restriction enzymes. This intermediate construct was known as ph8SPmGluR4//CaR(no stop). In the final cloning step, a fragment containing the Gα_qi5 cDNA was released from phmGluR8//CaR*AAA*Gα_qi5 using the restriction enzymes ApaI and NotI (both New England Biolabs) and subcloned into the ph8SPmGluR4//CaR(no stop) construct, which was prepared with the same restriction enzymes. The sequence of the resultant chimeric construct, ph8SPmGluR4//CaR*AAA*Gα_qi5, was verified by ABI automated DNA sequence analysis.

VIII. phmGluR8//CaR Construct

This chimera contains the extracellular and transmembrane domains of human mGluR8 linked to the intracellular cytoplasmic tail domain of the human CaR. The

chimeric junction between hmGluR8 and the CaR was created using a recombinant PCR strategy similar to those described above.

The first reaction used two primers, CH5A (sense 19-mer, corresponding to nucleotides 2187-2205 of human mGluR8, Stormann *et al.,* U.S. Patent Nos. 6,051,688, 6,077,675, and 6,084,084) and the hybrid primer CH5B (antisense 40-mer, containing 22 nucleotides complementary to nucleotides 2523 – 2544 of human mGluR8, and 18 nucleotides complementary to nucleotides 2602-2619 of the human CaR). These primers were used to amplify a 375 bp PCR fragment of human mGluR8. In a separate PCR reaction using phCaR in the BlueScript SK(-) plasmid as template, a 750 bp fragment of the human CaR was amplified using a hybrid primer CH5C (sense 40-mer, exactly complementary to primer CH5B) and the T3 primer commercially available from Stratagene.

The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers CH5A and T3, and the Pfu DNA polymerase (Stratagene). The resulting chimeric PCR product was digested with BsrG I and Xba I (New England Biolabs) and subcloned into pmGluR8 digested with the same two restriction enzymes. The sequence of the resultant chimeric construct, pmGluR8//CaR, was verified by DNA sequence analysis.

IX. mGluR8//CaR*Gα_qi5 Construct

This construct contains the hmGluR8//CaR chimeric receptor fused to human Gα_qi5. The chimeric junction between the C-terminus of hmGluR8//CaR and the N-terminus of Gα_qi5 was created using a recombinant PCR strategy similar to that described above for the construction of phmGluR2//CaR*Gα_qi5.

The first reaction used two primers, CRP10A (sense 18-mer, corresponding to nucleotides 2812-2829 of phCaR) and the hybrid primer Gqi5/CaR (antisense 40-mer, containing 21 nucleotides complementary to nucleotides 3214-3234 phCaR, and 19 nucleotides complementary to nucleotides 1-19 of pGα_qi5). These primers were used to amplify a 441 bp PCR fragment of hmGluR8//CaR.

In a separate PCR reaction all of Gα_qi5 was amplified using a hybrid primer CaR/Gqi5 (sense 40-mer, exactly complementary to primer Gqi5/CaR) and the Apa I-mut primer (20-mer). The two PCR products generated from the above two reactions were

annealed together in equimolar ratios in the presence of the external primers CRP10A and Apa I-mut, and the Pfu DNA polymerase (Stratagene).

The resulting chimeric PCR product was digested with BstE II and Apa I (New England Biolabs) and subcloned into pmGluR8//CaR digested with the same two restriction enzymes. The sequence of the resultant chimeric fusion construct, pmGluR8//CaR*Gα_qi5, was verified by DNA sequence analysis.

Example 2: Functional Expression of CaR/GABA$_B$R2

In vitro transcribed RNA (7 ng) encoding a chimeric CaR/GABA$_B$R2 (CaR extracellular and transmembrane domains, and intracellular GABA$_B$R2 domain) was co-injected with *in vitro* transcribed RNA (2 ng) encoding G 15 into *Xenopus* oocytes. Following a 72-hour incubation, the oocytes were voltage-clamped using standard electrophysiological techniques (Hille, B., Ionic Channels of Exictable Membranes, pp.30-33, Sinauer Associates, Inc., Sunderland, Ma., 1992). Activation of the chimeric receptor was detected by increases in the calcium-activated chloride current.

Application of the CaR activator 100 Gd^{3+}, resulted in reversible, oscillatory increases in the calcium-activated chloride current as shown in Figure 8. These data demonstrate the functional response of the chimeric CaR/GABA$_B$R2 receptor upon activation via a site within the CaR extracellular domain. In this assay, the G 15 subunit acts to promote signal transduction through intracellular pathways that mobilize intracellular Ca^{++}.

Example 3: Expression of Different G-Protein Fusion Receptors

The ability of different G-protein fusions to transduce signal resulting from ligand binding is shown in Figure 15. The different G-protein fusion receptors used in this example were as follows: mGluR2//CaR*Gqi5 (SEQ. ID. NO. 37), CaR/mGluR2*Gqi5 (SEQ. ID. NO. 33), and mGluR8//CaR*Gqi5 SEQ. ID. NO. 41.

Oocytes suitable for injection were obtained from adult female Xenopus laevis toads using procedures described in C. J. Marcus-Sekura and M. J. M. Hitchcock, Methods in Enzymology, Vol. 152 (1987).

Receptor fusion cRNAs were dissolved in water and 50 nl (12.5 ng/oocyte) were injected into individual oocytes. Following injection, oocytes were incubated at 16°C in MBS containing 1 mM $CaCl_2$ for 2 to 7 days prior to electrophysiological recording.

Test substances were applied by superfusion at a flow rate of about 5 ml/min. Receptor fusion activation was determined by measuring the increase in calcium-activated chloride current (I_{Cl}). Increases in I_{Cl} were quantified by measuring the peak inward current stimulated by activating agent, relative to the holding current at -60 mV. Application of 100 μM L-glutamate elicited a response from the mGluR2//CaR*Gαqi5 and mGluR8//CaR*Gαqi5. Application of 100 μM Gd^{3+} activated the CaR/mGluR2*Gqi5.

Example 4: Expression of Different G-Protein Fusion Receptors in Mammalian Cells

HEK293 cells were transiently transfected with the p8SPhmGluR4//CaR*AAA*Gαqi5 or phmGluR8//CaR*Gαqi5 plasmid DNAs using the following protocol. Initially, 150 cm^2 tissue culture flasks containing HEK293 cells at 75% confluence were transfected with 24 ug of plasmid DNA using Gibco BRL Life Technologies' Lipofectamine reagent. Following liposomal gene delivery the cells were allowed to recover for 24 hours. They were then plated overnight at 100,000 cells per well in black, clear bottom, Collagen I coated 96-well plates (Becton Dickenson, Biocoat) using DMEM supplemented with 10% fetal bovine serum (Hyclone Laboratories). The cells were assayed for function 48 hours after transient tranfection.

On the day of the assay, tissue culture medium was aspirated from the wells of a 96-well plate and 80 μL of Assay Buffer (Assay Buffer is: 20 mM HEPES, 146 mM NaCl, 5 mM KCl, 1 mM $MgCl_2$, 1 mM $CaCl_2$, 1 mg/ml BSA, 1 mg/ml glucose, pH 7.4) supplemented with 6 μM of the Ca^{2+}-sensitive dye, Fluo-3 AM (Molecular Probes) and 0.025% Pluronic (Molecular Probes) was added to each well.

The plate was then incubated in the dark for 1 hour at room temperature to efficiently load the cells with Fluo-3. At the end of the incubation, extracellular Fluo-3 was removed by washing the plate with Assay Buffer. Assay Buffer was added back to each well (final volume = 160 μL) prior to beginning the assay. The plate was loaded into a fluorescence imaging plate reader (FLIPR) robotic device (Molecular Devices) with the laser setting at 0.8 Watts. At a time of 15 seconds after initiation of the assay, 40 μL of Assay Buffer containing 150 μM L-AP4 was added to the 160 μL of Assay Buffer in each well of the plate to yield a final concentration of 30 μM L-AP4.

Relative fluorescence intensity (excitation $\lambda = 488$ nm / emission $\lambda = 510$ nm) was monitored at relevant time intervals throughout the assay period to measure L-AP4-induced receptor activation.

Other embodiments are within the following claims. Thus, while several embodiments have been shown and described, various modifications may be made, without departing from the spirit and scope of the present invention.

Claims

1. A G-protein fusion receptor comprising

an extracellular domain comprising an extracellular domain amino acid sequence substantially similar to either an extracellular CaR amino acid sequence, an extracellular mGluR amino acid sequence, or an extracellular $GABA_B$ receptor amino acid sequence;

a transmembrane domain joined to the carboxy terminus of said extracellular domain, said transmembrane domain comprising a transmembrane domain amino acid sequence substantially similar to either a transmembrane CaR amino acid sequence, a transmembrane mGluR amino acid sequence, or a transmembrane $GABA_B$ receptor amino acid sequence;

an intracellular domain joined to the carboxy terminus of said transmembrane domain comprising all or a portion of an intracellular amino acid sequence substantially similar to either an intracellular CaR amino acid sequence, an intracellular mGluR amino acid sequence, or an intracellular $GABA_B$ receptor amino acid sequence, provided that said portion is at least about 10 amino acids;

an optionally present linker joined to the carboxy terminus of said intracellular domain; and

a G-protein joined either to said intracellular domain or to said optionally present linker, provided that said G-protein is joined to said optionally present linker when said optionally present linker is present.

2. The G-protein fusion receptor of claim 1, wherein said extracellular domain consists of said extracellular domain amino acid sequence, said transmembrane domain consists of said transmembrane domain amino acid sequence; and said intracellular domain consists of said transmembrane domain amino acid sequence.

3. The G-protein fusion receptor of claim 2, wherein said optionally present linker is present and is a polypeptide 3 to 30 amino acids in length.

4. The G-protein fusion receptor of claim 2, wherein said optionally present linker is not present.

5. 1. The G-protein fusion receptor of claim 3 or 4, wherein said G-protein is selected from the group consisting of: G_{15}, G_{16}, Gqo5, and Gqi5

6. The G-protein fusion of claim 5, wherein any of said CaR sequence present is a human CaR sequence, any of said mGluR sequence present is from a human mGluR, and any of said $GABA_B$ receptor sequence present is from human mGluR.

7. A nucleic acid comprising a nucleotide sequence encoding for the G-protein fusion of any one of claims 1-6.

8. An expression vector comprising a nucleotide sequence encoding for the G-protein fusion of any one of claims 1-6 transcriptionally coupled to a promoter.

9. A recombinant cell comprising the expression vector of claim 8 and a cell wherein the G-protein fusion is expressed and is functional.

10. A recombinant cell produced by combining a vector comprising the nucleic acid of claim 9 and elements for introducing heterologous nucleic acid into a cell wherein the G-protein fusion receptor is expressed, and said cell.

11. A process for the production of a G-protein fusion receptor comprising:

growing procaryotic or eukaryotic host cells comprising a nucleic acid sequence expressing the G-protein fusion receptor of any one of claims 1-6, under suitable nutrient conditions allowing for cell growth.

12. A method of measuring the ability of a compound to effect G-protein fusion activity comprising the steps of:

a) providing said compound to a cell expressing the G-protein fusion receptor of any one of claims 1-6, and

b) measuring the ability of said compound to affect the activity of said receptor as an indication of the ability of said compound to effect G-protein fusion receptor activity.

13. A chimeric receptor comprising

an extracellular domain comprising an extracellular domain amino acid sequence substantially similar to a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4 and SEQ ID NO: 5;

a transmembrane domain comprising a transmembrane domain amino acid sequence substantially similar to a sequence selected from the group consisting of SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, and SEQ ID NO: 10; and

an intracellular cytoplasmic domain comprising an intracellular domain amino acid sequence substantially similar to a sequence selected from the group consisting of SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, and SEQ ID NO: 14;

wherein at least one domain is present which comprises an amino acid sequence substantially similar to a sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 7, SEQ ID NO: 8, and SEQ ID NO: 9, SEQ ID NO: 12, SEQ ID NO: 13, and SEQ ID NO: 14; and at least one domain is present which comprises an amino acid sequence substantially similar to a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 11, and SEQ ID NO: 15.

14. The chimeric receptor of claim 13 wherein said extracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 3, and 4; said transmembrane domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID Nos: 6, 7, 8, 9, and 10; and said intracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 11 and 15.

15. The chimeric receptor of claim 14, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 2; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence SEQ ID NO: 7; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 11.

16. The chimeric receptor of claim 14, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 3; said

transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 8; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO 11.

17. The chimeric receptor of claim 14, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence SEQ ID NO: 4; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 9; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO 11.

18. The chimeric receptor of claim 13, wherein said extracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 2, 3, 4 and 5; said transmembrane domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID Nos: 7, 8, and 9; and said intracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 11, 12, 13, 14, and 15.

19. The chimeric receptor of claim 18, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 7; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 11.

20. The chimeric receptor of claim 18, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 8; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO 11.

21. The chimeric receptor of claim 18, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid

sequence of SEQ ID NO: 9; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO 11.

22. The chimeric receptor of claim 13, wherein said extracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 2, 3, 4, and 5; said transmembrane domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID Nos: 6, 7, 8, 9, and 10; and said intracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 12, 13, and 14.

23. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 6; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 12.

24. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 7; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 12.

25. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 8; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 13.

26. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid

sequence of SEQ ID NO: 6; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 13.

27. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 9; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 14.

28. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 6; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 14.

29. The chimeric receptor of any one of claims 13-28, wherein said receptor functional couples to a G-protein.

30. The chimeric receptor of any one of claims 13-28, wherein said chimeric receptor consists of said extracelluar domain, said transmembrane domain, said intracellular domain, and an optionally present G-protein α subunit covalently joined to said intracellular domain.

31. The chimeric receptor of claim 30, wherein said chimeric receptor consists of said extracelluar domain, said transmembrane domain, and said intracellular domain.

32. The chimeric receptor of claim 30, wherein said G-protein α subunit consists of the amino acid sequence of SEQ ID Nos: 16 or 17.

33. A nucleic acid comprising a nucleotide sequence encoding for the chimeric receptor of any one of claims 13-32.

34. An expression vector comprising a nucleotide sequence encoding for the chimeric receptor of any one of claims 13-32 transcriptionally coupled to a promoter.

35. A recombinant cell comprising the expression vector of claim 34 and a cell wherein the chimeric receptor is expressed and is functional.

36. A recombinant cell produced by combining a vector comprising the nucleic acid of claim 33 and elements for introducing heterologous nucleic acid into a cell wherein the chimeric receptor is expressed, and said cell.

37. A process for the production of a chimeric receptor comprising:

growing procaryotic or eukaryotic host cells comprising a nucleic acid sequence expressing the chimeric receptor of any one of claims 13-32, under suitable nutrient conditions allowing for cell growth.

38. A method of measuring the ability of a compound to effect $GABA_BR$ or mGluR activity comprising the steps of:

a) providing said compound to a cell expressing the chimeric receptor of any one of claims 13-32, and

b) measuring the ability of said compound to affect the activity of said receptor as an indication of the ability of said compound to effect $GABA_BR$ or mGluR activity.

39. The method of claim 38, wherein said method measures activity at a $GABA_BR$.

40. The method of claim 38, wherein said method measures activity at a mGluR.

41. A fusion receptor polypeptide comprising a receptor and a G-protein α subunit, wherein said G-protein α subunit is fused to the intracellular domain of said receptor, provided that said receptor is not an adrenoreceptor.

ABSTRACT

The present invention features G-protein fusion receptors and chimeric $GABA_B$ receptors ($GABA_BRs$), nucleic acid encoding such receptors, and the use of such receptors and nucleic acid. G-protein fusion receptors comprise at least one domain from a CaR, a mGluR, and/or a $GABA_B$ receptor fused directly or through a linker to a guanine nucleotide-binding protein (G-protein). Chimeric $GABA_BRs$ comprise at least one of a $GABA_BR$ extracellular domain, a $GABA_BR$ transmembrane domain, or a $GABA_BR$ intracellular domain and one or more domains from a mGluR subtype 8 (mGluR8) and/or a CaR.

ClustalW Formatted Alignments

SEQ ID 1	M A F Y S C C W V L L A L T W H T S A Y G P D Q R
SEQ ID 2	M L L L L L L A P L F L R P P G A G G A Q T P N A
SEQ ID 3	M G P G A P F A R V G W P L P L L V V M A A G V A
SEQ ID 4	M A S P R S S G Q P G P X P P P P P P P A R L L L
SEQ ID 5	M V C E G K R S A S C P C F F L L T A K F Y W I L

SEQ ID 1	A Q K K G D I I L G G L F P I H F G V A A K D Q D
SEQ ID 2	T S E G C Q I I H P P W E G G I R Y R G L T R D Q
SEQ ID 3	P V W A S H S P H L P R P H S R V P P H P S S E R
SEQ ID 4	L L L L P L L L P L A P G A W G W A R G A P R P P
SEQ ID 5	T M M Q R T H S Q E Y A H S I R V D G D I I L G G

SEQ ID 1	L K S R P E S V E C I R Y N F R G F R W L Q A M I
SEQ ID 2	V K A I N F L P V D Y E I E Y V C R G E R E V V G
SEQ ID 3	R A V Y I G A L F P M S G G W P G G Q A C Q P A V
SEQ ID 4	P S S P P L S I M G L M P L T K E V A K G S I G R
SEQ ID 5	L F P V H A K G E R G V P C G E L K K E K G I H R

SEQ ID 1	F A I E E I N S S P A L L P N L T L G Y R I F D T
SEQ ID 2	P K V R K C L A N G S W T D M D T P S R C V R I C
SEQ ID 3	E M A L E D V N S R R D I L P D Y E L K L I H H D
SEQ ID 4	G V L P A V E L A I E Q I R N E S L L R P Y F L D
SEQ ID 5	L E A M L Y A I D Q I N K D P D L L S N I T L G V

SEQ ID 1	C N T V S K A L E A T L S F V A Q N K I D S L N L
SEQ ID 2	S K S Y L T L E N G K V F L T G G D L P A L D G A
SEQ ID 3	S K C D P G Q A T K Y L Y E L L Y N D P I K I I L
SEQ ID 4	L R L Y D T E C D N A K G L K A F Y D A I K Y G P
SEQ ID 5	R I L D T C S R D T Y A L E Q S L T F V Q A L I E

SEQ ID 1	D E F C N C S E H I P S T I A V V G A T G S G V S
SEQ ID 2	R V D F R C D P D F H L V G S S R S I C S Q G Q W
SEQ ID 3	M P G C S S V S T L V A E A A R M W N L I V L S Y
SEQ ID 4	N H L M V F G G V C P S V T S I I A E S L Q G W N
SEQ ID 5	K D A S D V K C A N G D P P I F T K P D K I S G V

SEQ ID 1	T A V A N L L G L F Y I P Q V S Y A S S S R L L S
SEQ ID 2	S T P K P H C Q V N R T P H S E R R A V Y I G A L
SEQ ID 3	G S S S P A L S N R Q R F P T F F R T H P S A T L
SEQ ID 4	L V Q L S F A A T T P V L A D K K K Y P Y F F R T
SEQ ID 5	I G A A A S S V S I M V A N I L R L F K I P Q I S

Figure 1a

SEQ ID 1	N K N Q F K S F L R T I P N D E H Q A T A M A D I
SEQ ID 2	F P M S G G W P G G Q A C Q P A V E M A L E D V N
SEQ ID 3	H N P T R V K L F E K W G W K K I A T I Q Q T T E
SEQ ID 4	V P S D N A V N P A I L K L L K H Y Q W K R V G T
SEQ ID 5	Y A S T A P E L S D N T R Y D F F S R V V P P D S

SEQ ID 1	I E Y F R W N W V G T I A A D D D Y G R P G I E K
SEQ ID 2	S R R D I L P D Y E L K L I H H D S K C D P G Q A
SEQ ID 3	V F T S T L D D L E E R V K E A G I E I T F R Q S
SEQ ID 4	L T Q D V Q R F S E V R N D L T G V L Y G E D I E
SEQ ID 5	Y Q A Q A M V D I V T A L G W N Y V S T L A S E G

SEQ ID 1	F R E E A E E R D I C I D F S E L I S Q Y S D E E
SEQ ID 2	T K Y L Y E L L Y N D P I K I I L M P G C S S V S
SEQ ID 3	F F S D P A V P V K N L K R Q D A R I I V G L F Y
SEQ ID 4	I S D T E S F S N D P C T S V K K L K G N D V R I
SEQ ID 5	N Y G E S G V E A F T Q I S R E I G G V C I A Q S

SEQ ID 1	E I Q H V V E V I Q N S T A K V I V V F S S G P D
SEQ ID 2	T L V A E A A R M W N L I V L S Y G S S S P A L S
SEQ ID 3	E T E A R K V F C E V Y K E R L F G K K Y V W F L
SEQ ID 4	I L G Q F D Q N M A A K V F C C A Y E E N M Y G S
SEQ ID 5	Q K I P R E P R P G E F E K I I K R L L E T P N A

SEQ ID 1	L E P L I K E I V R R N I T G K I W L A S E A W A
SEQ ID 2	N R Q R F P T F F R T H P S A T L H N P T R V K L
SEQ ID 3	I G W Y A D N W F K I Y D P S I N C T V D E M T E
SEQ ID 4	K Y Q W I I P G W Y E P S W W E Q V H T E A N S S
SEQ ID 5	R A V I M F A N E D D I R R I L E A A K K L N Q S

SEQ ID 1	S S S L I A M P Q Y F H V V G G T I G F A L K A G
SEQ ID 2	F E K W G W K K I A T I Q Q T T E V F T S T L D D
SEQ ID 3	A V E G H I T T E I V M L N P A N T R S I S N M T
SEQ ID 4	R C L R K N L L A A M E G Y I G V D F E P L S S K
SEQ ID 5	G H F L W I G S D S W G S K I A P V Y Q Q E E I A

SEQ ID 1	Q I P G F R E F L K K V H P R K S V H N G F A K E
SEQ ID 2	L E E R V K E A G I E I T F R Q S F F S D P A V P
SEQ ID 3	S Q E F V E K L T K R L K R H P E E T G G F Q E A
SEQ ID 4	Q I K T I S G K T P Q Q Y E R E Y N N K R S G V G
SEQ ID 5	E G A V T I L P K R A S I D G F D R Y F R S R T L

Figure 1b

SEQ ID 1	F W E E T F N C H L Q E G A K G P L P V D T F L R
SEQ ID 2	V K N L K R Q D A R I I V G L F Y E T E A R K V F
SEQ ID 3	P L A Y D A I W A L A L A L N K T S G G G G R S G
SEQ ID 4	P S K F H G Y A Y D G I W V I A K T L Q R A M E T
SEQ ID 5	A N N R R N V W F A E F W E E N F G C K L G S H G

SEQ ID 1	G H E E S G D R F S N S S T A F R P L C T G D E N
SEQ ID 2	C E V Y K E R L F G K K Y V W F L I G W Y A D N W
SEQ ID 3	V R L E D F N Y N N Q T I T D Q I Y R A M N S S S
SEQ ID 4	L H A S S R H Q R I Q D F N Y T D H T L G R I I L
SEQ ID 5	K R N S H I K K C T G L E R I A R D S S Y E Q E G

SEQ ID 1	I S S V E T P Y I D Y T H L R I S Y N V Y L A V Y
SEQ ID 2	F K I Y D P S I N C T V D E M T E A V E G H I T T
SEQ ID 3	F E G V S G H V V F D A S G S R M A W T L I E Q L
SEQ ID 4	N A M N E T N F F G V T G Q V V F R N G E R M G T
SEQ ID 5	K V Q F V I D A V Y S M A Y A L H N M H K D L C P

SEQ ID 1	S I A H A L Q D I Y T C L P G R G L F T N G S C A
SEQ ID 2	E I V M L N P A N T R S I S N M T S Q E F V E K L
SEQ ID 3	Q G G S Y K K I G Y Y D S T K D D L S W S K T D K
SEQ ID 4	I K F T Q F Q D S R E V K V G E Y N A V A D T L E
SEQ ID 5	G Y I G L C P R M S T I D G K E L L G Y I R A V N

SEQ ID 1	D I K K V E A W Q V L K H L R H L N F T N N M G E
SEQ ID 2	T K R L K R H P E E T G G F Q E A P L A Y D A I W
SEQ ID 3	W I G G S P P A D Q T L V I K T F R F L S Q K
SEQ ID 4	I I N D T I R F Q G S E P P K D K T I I L E Q L R
SEQ ID 5	F N G S A G T P V T F N E N G D A P G R Y D I F Q

SEQ ID 1	Q V T F D E C G D L V G N Y S I I N W H L S P E D
SEQ ID 2	A L A L A L N K T S G G G G R S G V R L E D F N Y
SEQ ID 3	
SEQ ID 4	K I S L P
SEQ ID 5	Y Q I T N K S T E Y K V I G H W T N Q L H L K V E

SEQ ID 1	G S I V F K E V G Y Y N V Y A K K G E R L F I N E
SEQ ID 2	N N Q T I T D Q I Y R A M N S S S F E G V S G H V
SEQ ID 3	
SEQ ID 4	
SEQ ID 5	D M Q W A H R E H T H P A S V C S L P C K P G E R

Figure 1c

SEQ ID 1	E K I L W S G F S R E V P F S N C S R D C L A G T
SEQ ID 2	V F D A S G S R M A W T L I E Q L Q G G S Y K K I
SEQ ID 3	
SEQ ID 4	
SEQ ID 5	K K T V K G V P C C W H C E R C E G Y N Y Q V D E

SEQ ID 1	R K G I I E G E P T C C F E C V E C P D G E Y S D
SEQ ID 2	G Y Y D S T K D D L S W S K T D K W I G G S P P A
SEQ ID 3	
SEQ ID 4	
SEQ ID 5	L S C E L C P L D Q R P N M N R T G C Q L I P I I

SEQ ID 1	E T D A S A C N K C P D D F W S N E N H T S C I A
SEQ ID 2	D Q T L V I K T F R F L S Q K
SEQ ID 3	
SEQ ID 4	
SEQ ID 5	K L E W H S P W

SEQ ID 1	K E I E F L S W T E P F
SEQ ID 2	
SEQ ID 3	
SEQ ID 4	
SEQ ID 5	

Figure 1d

FIGURE 2a

SEQ ID 6	G I A L T L F A V L G I F L T A F V L G V F I K F R N T P I
SEQ ID 7	L F I S V S V L S S L G I V L A V V C L S F N I Y N S H V R
SEQ ID 8	L F I S V S V L S S L G I V L A V V C L S F N I Y N S H V R
SEQ ID 9	L Y S I L S A L T I L G M I M A S A F L F F N I K N R N Q K
SEQ ID 10	A V V P V F V A I L G I I A T T F V I V T F V R Y N D T P I
SEQ ID 6	V K A T N R E L S Y L L L F S L L C C F S S S L F F I G E P
SEQ ID 7	Y I Q N S Q P N L N N L T A V G C S L A L A A V F P L G L D
SEQ ID 8	Y I Q N S Q P N L N N L T A V G C S L A L A A V F P L G L D
SEQ ID 9	L I K M S S P Y M N N L I I L G G M L S Y A S I F L F G L D
SEQ ID 10	V R A S G R E L S Y V L L T G I F L C Y S I T F L M I A A P
SEQ ID 6	Q D W T C R L R Q P A F G I S F V L C I S C I L V K T N R V
SEQ ID 7	G Y H I G R N Q F P F V C Q A R L W L L G L G F S L G Y G S
SEQ ID 8	G Y H I G R N Q F P F V C Q A R L W L L G L G F S L G Y G S
SEQ ID 9	G S F V S E K T F E T L C T V R T W I L T V G Y T T A F G A
SEQ ID 10	D T I I C S F R R V F L G L G M C F S Y A A L L T K T N R I
SEQ ID 6	L L V F E A K I P T S F H R K W W G L N L Q F L L V F L C T
SEQ ID 7	M F T K I W W V H T V F T K K E E K K E W R K T L E P W K L
SEQ ID 8	M F T K I W W V H T V F T K K E E K K E W R K T L E P W K L
SEQ ID 9	M F A K T W R V H A I F K N V K M K K K I I K D Q K L L V I
SEQ ID 10	H R I F E Q G K K S V T A P K F I S P A S Q L V I T F S L I
SEQ ID 6	F M Q I V I C V I W L Y T A P P S S Y R N Q E L E D E I I F
SEQ ID 7	Y A T V G L L V G M D V L T L A I W Q I V D P L H R T I E T
SEQ ID 8	Y A T V G L L V G M D V L T L A I W Q I V D P L H R T I E T
SEQ ID 9	V G G M L L I D L C I L I C W Q A V D P L R R T V E K Y S M
SEQ ID 10	S V Q L L G V F V W F V V D P P H I I I D Y G E Q R T L D P
SEQ ID 6	I T C H E G S L M A L G F L I G Y T C L L A A I C F F F A F
SEQ ID 7	F A K E E P K E D I D V S I L P Q L E H C S S R K M N T W L
SEQ ID 8	F A K E E P K E D I D V S I L P Q L E H C S S R K M N T W L
SEQ ID 9	E P D P A G R D I S I R P L L E H C E N T H M T I W L G I V
SEQ ID 10	E K A R G V L K C D I S D L S L I C S L G Y S I L L M V T C
SEQ ID 6	K S R K L P E N F N E A K F I T F S M L I F F I V W I S F I
SEQ ID 7	G I F Y G Y K G L L L L L G I F L A Y E T K S V S T E K I N
SEQ ID 8	G I F Y G Y K G L L L L L G I F L A Y E T K S V S T E K I N
SEQ ID 9	Y A Y K G L L M L F G C F L A W E T R N V S I P A L N D S K
SEQ ID 10	T V Y A I K T R G V P E T F N E A K P I G F T M Y T T C I I

FIGURE 2L

SEQ ID 6	P A Y A S T Y G K F V S A V E V I A I L A A S F G L L A C I
SEQ ID 7	D H R A V G M A I Y N V A V L C L I T A P V T M I L S S Q Q
SEQ ID 8	D H R A V G M A I Y N V A V L C L I T A P V T M I L S S Q Q
SEQ ID 9	Y I G M S V Y N V G I M C I I G A A V S F L T R D Q P N V Q
SEQ ID 10	W L A F I P I F F G T A Q S A E K M Y I Q T T T L T V S M S

SEQ ID 6	F F N K I Y I I L F
SEQ ID 7	D A A F A F A S L A I V F S S Y I T L V V L F V P K M
SEQ ID 8	D A A F A F A S L A I V F S S Y I T L V V L F V P K M
SEQ ID 9	F C I V A L V I I F C S T I T L C L V F V P K L
SEQ ID 10	L S A S V S L G M L Y M P K V Y I I I F

FIGURE 3a

SEQ ID 11	K P S R N T I E E V R C S T A A H A F K V A A R A T L R R S
SEQ ID 12	R R L I T R G E W Q S E A Q D T M K T G S S T N N N E E E K
SEQ ID 13	R R L I T R G E W Q S E A Q D T M K T G S S T N N N E E E K
SEQ ID 14	I T L R T N P D A A T Q N R R F Q F T Q N Q K K E D S K T S
SEQ ID 15	H P E Q N V Q K R K R S F K A V V T A A T M Q S K L I Q K G

SEQ ID 11	N V S R K R S S S L G G S T G S T P S S S I S S K S N S E D
SEQ ID 12	S R L L E K E N R E L E K I I A E K E E R V S E L R H Q L Q
SEQ ID 13	S R L L E K E N R E L E K I I A E K E E R V S E L R H Q L Q
SEQ ID 14	T S V T S V N Q A S T S R L E G L Q S E N H R L R M K I T E
SEQ ID 15	N D R P N G E V K S E L C E S L E T N S K S S V E F P M V K

SEQ ID 11	P F P Q P E R Q K Q Q Q P L A L T Q Q E Q Q Q P L T L P Q
SEQ ID 12	S R Q Q L R S R R H P P T P P E P S G G L P R G P P E P P D
SEQ ID 13	S R Q Q L R S R R H P P T P P E P S G G L P R G P P E P P D
SEQ ID 14	L D K D L E E V T M Q L Q D T P E K T T Y I K Q N H Y Q E L
SEQ ID 15	S G S T S

SEQ ID 11	Q Q R S Q Q Q P R C K Q K V I F G S G T V T F S L S F D E P
SEQ ID 12	R L S C D G S R V H L L Y K
SEQ ID 13	R L S C D G S R V H L L Y K
SEQ ID 14	N D I L N L G N F T E S T D G G K A I L K N H L D Q N P Q L
SEQ ID 15	

SEQ ID 11	Q K N A M A H G N S T H Q N S L E A Q K S S D T L T R H Q P
SEQ ID 12	
SEQ ID 13	
SEQ ID 14	Q W N T T E P S R T C K D P I E D I N S P E H I Q R R L S L
SEQ ID 15	

SEQ ID 11	L L P L Q C G E T D L D L T V Q E T G L Q G P V G G D Q R P
SEQ ID 12	
SEQ ID 13	
SEQ ID 14	Q L P I L H H A Y L P S I G G V D A S C V S P C V S P T A S
SEQ ID 15	

SEQ ID 11	E V E D P E E L S P A L V V S S S Q S F V I S G G G S T V T
SEQ ID 12	
SEQ ID 13	
SEQ ID 14	P R H R H V P P S F R V M V S G L
SEQ ID 15	

FIGURE 3

SEQ ID 11 E N V V N S
SEQ ID 12
SEQ ID 13
SEQ ID 14
SEQ ID 15

FIGURE 4a

SEQ. ID. NO. 16	M A R S L T W G C C P W C L T E E E K T A A R I D Q E I N R
SEQ. ID. NO. 17	M A R S L T W R C C P W C L T E D E K A A A R V D Q E I N R
SEQ. ID. NO. 16	I L L E Q K K Q E R E E L K L L L L G P G E S G K S T F I K
SEQ. ID. NO. 17	I L L E Q K K Q D R G E L K L L L L G P G E S G K S T F I K
SEQ. ID. NO. 16	Q M R I I H G V G Y S E E D R R A F R L L I Y Q N I F V S M
SEQ. ID. NO. 17	Q M R I I H G A G Y S E E E R K G F R P L V Y Q N I F V S M
SEQ. ID. NO. 16	Q A M I D A M D R L Q I P F S R P D S K Q H A S L V M T Q D
SEQ. ID. NO. 17	R A M I E A M E R L Q I P F S R P E S K H H A S L V M S Q D
SEQ. ID. NO. 16	P Y K V S T F E K P Y A V A M Q Y L W R D A G I R A C Y E R
SEQ. ID. NO. 17	P Y K V T T F E K R Y A A A M Q W L W R D A G I R A C Y E R
SEQ. ID. NO. 16	R R E F H L L D S A V Y Y L S H L E R I S E D S Y I P T A Q
SEQ. ID. NO. 17	R R E F H L L D S A V Y Y L S H L E R I T E E G Y V P T A Q
SEQ. ID. NO. 16	D V L R S R M P T T G I N E Y C F S V K K T K L R I V D V G
SEQ. ID. NO. 17	D V L R S R M P T T G I N E Y C F S V Q K T N L R I V D V G
SEQ. ID. NO. 16	G Q R S E R R K W I H C F E N V I A L I Y L A S L S E Y D Q
SEQ. ID. NO. 17	G Q K S E R K K W I H C F E N V I A L I Y L A S L S E Y D Q
SEQ. ID. NO. 16	C L E E N D Q E N R M E E S L A L F S T I L E L P W F K S T
SEQ. ID. NO. 17	C L E E N N Q E N R M K E S L A L F G T I L E L P W F K S T
SEQ. ID. NO. 16	S V I L F L N K T D I L E D K I H T S H L A T Y F P S F Q G
SEQ. ID. NO. 17	S V I L F L N K T D I L E E K I P T S H L A T Y F P S F Q G
SEQ. ID. NO. 16	P R R D A E A A K S F I L D M Y A R V Y A S C A E P Q D G G
SEQ. ID. NO. 17	P K Q D A E A A K R F I L D M Y T R M Y T G C V D G P E G S
SEQ. ID. NO. 16	R K G S R A R R F F A H F T C A T D T Q S V R S V F K D V R
SEQ. ID. NO. 17	K K G A R S R R L F S H Y T C A T D T Q N I R K V F K D V R

FIGURE 4b

SEQ. ID. NO. 16	D	S	V	L	A	R	Y	L	D	E	I	N	L	L
SEQ. ID. NO. 17	D	S	V	L	A	R	Y	L	D	E	I	N	L	L

ClustalW Formatted Alignments

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SEQ. ID. NO. 18  A T G G C A T T T T A T A G C T G C T G C T G G G
SEQ. ID. NO. 19  A T G T T G C T G C T G C T G C T A C T G G C G C
SEQ. ID. NO. 20  A T G G G G C C C G G G G C C C C T T T T G C C C
SEQ. ID. NO. 21  A T G G C T T C C C C G C G G A G C T C C G G G C

SEQ. ID. NO. 18  T C C T C T T G G C A C T C A C C T G G C A C A C
SEQ. ID. NO. 19  C A C T C T T C C T C C G C C C C C C G G G C G C
SEQ. ID. NO. 20  G G G T G G G G T G G C C A C T G C C G C T T C T
SEQ. ID. NO. 21  A G C C C G G G C C G C - G C C G C C G C C G C C

SEQ. ID. NO. 18  C T C T G C C T A C G G G C C A G A C C A G C G A
SEQ. ID. NO. 19  G G G C G G G G C G C A G A C C C C C A A C G C C
SEQ. ID. NO. 20  G G T T G T G A T G G C G G C A G G G G T G G C T
SEQ. ID. NO. 21  A C C G C C G C C C G C G C G C C T G C T A C T G

SEQ. ID. NO. 18  G C C C A A A A G A A G G G G G A C A T T A T C C
SEQ. ID. NO. 19  A C C T C A G A A G G T T G C C A G A T C A T A C
SEQ. ID. NO. 20  C C G G T G T G G G C C T C C C A C T C C C C C C
SEQ. ID. NO. 21  C T A C T G C T G C T G C C G C T G C T G C T G C

SEQ. ID. NO. 18  T T G G G G G G C T C T T T C C T A T T C A T T T
SEQ. ID. NO. 19  A C C C G C C C T G G G A A G G G G G C A T C A G
SEQ. ID. NO. 20  A T C T C C C G C G G C C T C A C T C G C G G G T
SEQ. ID. NO. 21  C T C T G G C G C C C G G G G C C T G G G G C T G

SEQ. ID. NO. 18  T G G A G T A G C A G C T A A A G A T C A A G A T
SEQ. ID. NO. 19  G T A C C G G G G C C T G A C T C G G G A C C A G
SEQ. ID. NO. 20  C C C C C C G C A C C C C T C C T C A G A A C G G
SEQ. ID. NO. 21  G G C G C G G G G C G C C C C C C G G C C G C C G

SEQ. ID. NO. 18  C T C A A A T C A A G G C C G G A G T C T G T G G
SEQ. ID. NO. 19  G T G A A G G C T A T C A A C T T C C T G C C A G
SEQ. ID. NO. 20  C G C G C A G T G T A C A T C G G G G C A C T G T
SEQ. ID. NO. 21  C C C A G C A G C C C G C C G C T C T C C A T C A

SEQ. ID. NO. 18  A A T G T A T C A G G T A T A A T T T C C G T G G
SEQ. ID. NO. 19  T G G A C T A T G A G A T T G A G T A T G T G T G
SEQ. ID. NO. 20  T T C C C A T G A G C G G G G G C T G G C C A G G
SEQ. ID. NO. 21  T G G G C C T C A T G C C G C T C A C C A A G G A
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Figure 5a

SEQ. ID. NO. 18 G T T T C G C T G G T T A C A G G C T A T G A T A
SEQ. ID. NO. 19 C C G G G G G G A G C G C G A G G T G G T G G G G
SEQ. ID. NO. 20 G G G C C A G G C C T G C C A G C C C G C G G T G
SEQ. ID. NO. 21 G G T G G C C A A G G G C A G C A T C G G G C G C

SEQ. ID. NO. 18 T T T G C C A T A G A G G A G A T A A A C A G C A
SEQ. ID. NO. 19 C C C A A G G T C C G C A A G T G C C T G G C C A
SEQ. ID. NO. 20 G A G A T G G C G C T G G A G G A C G T G A A T A
SEQ. ID. NO. 21 G G T G T G C T C C C C G C C G T G G A A C T G G

SEQ. ID. NO. 18 G C C C A G C C C T T C T T C C C A A C T T G A C
SEQ. ID. NO. 19 A C G G C T C C T G G A C A G A T A T G G A C A C
SEQ. ID. NO. 20 G C C G C A G G G A C A T C C T G C C G G A C T A
SEQ. ID. NO. 21 C C A T C G A G C A G A T C C G C A A C G A G T C

SEQ. ID. NO. 18 G C T G G G A T A C A G G A T A T T T G A C A C T
SEQ. ID. NO. 19 A C C C A G C C G C T G T G T C C G A A T C T G C
SEQ. ID. NO. 20 T G A G C T C A A G C T C A T C C A C C A C G A C
SEQ. ID. NO. 21 A C T C C T G C G C C C C T A C T T C C T C G A C

SEQ. ID. NO. 18 T G C A A C A C C G T T T C T A A G G C C T T G G
SEQ. ID. NO. 19 T C C A A G T C T T A T T T G A C C C T G G A A A
SEQ. ID. NO. 20 A G C A A G T G T G A T C C A G G C C A A G C C A
SEQ. ID. NO. 21 C T G C G G C T C T A T G A C A C G G A G T G C G

SEQ. ID. NO. 18 A A G C C A C C C T G A G T T T T G T T G C T C A
SEQ. ID. NO. 19 A T G G G A A G G T T T T C C T G A C G G G T G G
SEQ. ID. NO. 20 C C A A G T A C C T A T A T G A G C T G C T C T A
SEQ. ID. NO. 21 A C A A C G C A A A A G G G T T G A A A G C C T T

SEQ. ID. NO. 18 A A A C A A A A T T G A T T C T T T G A A C C T T
SEQ. ID. NO. 19 G G A C C T C C C A G C T C T G G A C G G A G C C
SEQ. ID. NO. 20 C A A C G A C C C T A T C A A G A T C A T C C T T
SEQ. ID. NO. 21 C T A C G A T G C A A T A A A A T A C G G G C C G

SEQ. ID. NO. 18 G A T G A G T T C T G C A A C T G C T C A G A G C
SEQ. ID. NO. 19 C G G G T G G A T T T C C G G T G T G A C C C C G
SEQ. ID. NO. 20 A T G C C T G G C T G C A G C T C T G T C T C C A
SEQ. ID. NO. 21 A A C C A C T T G A T G G T G T T T G G A G G C G

Figure 5b

SEQ. ID. NO. 18 A C A T T C C C T C T A C G A T T G C T G T G G T
SEQ. ID. NO. 19 A C T T C C A T C T G G T G G G C A G C T C C C G
SEQ. ID. NO. 20 C G C T G G T G G C T G A G G C T G C T A G G A T
SEQ. ID. NO. 21 T C T G T C C A T C C G T C A C A T C C A T C A T

SEQ. ID. NO. 18 G G G A G C A A C T G G C T C A G G C G T C T C C
SEQ. ID. NO. 19 G A G C A T C T G T A G T C A G G G C C A G T G G
SEQ. ID. NO. 20 G T G G A A C C T C A T T G T G C T T T C C T A T
SEQ. ID. NO. 21 T G C A G A G T C C C T C C A A G G C T G G A A T

SEQ. ID. NO. 18 A C G G C A G T G G C A A A T C T G C T G G G G C
SEQ. ID. NO. 19 A G C A C C C C C A A G C C C C A C T G C C A G G
SEQ. ID. NO. 20 G G C T C C A G C T C A C C A G C C C T G T C A A
SEQ. ID. NO. 21 C T G G T G C A G C T T T C T T T T G C T G C A A

SEQ. ID. NO. 18 T C T T C T A C A T T C C C C A G G T C A G T T A
SEQ. ID. NO. 19 T G A A T C G A A C G C C A C A C T C A G A A C G
SEQ. ID. NO. 20 A C C G G C A G C G T T T C C C C A C T T T C T T
SEQ. ID. NO. 21 C C A C G C C T G T T C T A G C C G A T A A G A A

SEQ. ID. NO. 18 T G C C T C C T C C A G C A G A C T C C T C A G C
SEQ. ID. NO. 19 G C G C G C A G T G T A C A T C G G G G C A C T G
SEQ. ID. NO. 20 C C G A A C G C A C C C A T C A G C C A C A C T C
SEQ. ID. NO. 21 A A A A T A C C C T T A T T T C T T T C G G A C C

SEQ. ID. NO. 18 A A C A A G A A T C A A T T C A A G T C T T T C C
SEQ. ID. NO. 19 T T T C C C A T G A G C G G G G G C T G G C C A G
SEQ. ID. NO. 20 C A C A A C C C T A C C C G C G T G A A A C T C T
SEQ. ID. NO. 21 G T C C C A T C A G A C A A T G C G G T G A A T C

SEQ. ID. NO. 18 T C C G A A C C A T C C C C A A T G A T G A G C A
SEQ. ID. NO. 19 G G G G C C A G G C C T G C C A G C C C G C G G T
SEQ. ID. NO. 20 T T G A A A A G T G G G G C T G G A A G A A G A T
SEQ. ID. NO. 21 C A G C C A T T C T G A A G T T G C T C A A G C A

SEQ. ID. NO. 18 C C A G G C C A C T G C C A T G G C A G A C A T C
SEQ. ID. NO. 19 G G A G A T G G C G C T G G A G G A C G T G A A T
SEQ. ID. NO. 20 T G C T A C C A T C C A G C A G A C C A C T G A G
SEQ. ID. NO. 21 C T A C C A G T G G A A G C G C G T G G G C A C G

Figure 5c

SEQ. ID. NO. 18 A T C G A G T A T T T C C G C T G G A A C T G G G
SEQ. ID. NO. 19 A G C C G C A G G G A C A T C C T G C C G G A C T
SEQ. ID. NO. 20 G T C T T C A C T T C G A C T C T G G A C G A C C
SEQ. ID. NO. 21 C T G A C G C A A G A C G T T C A G A G G T T C T

SEQ. ID. NO. 18 T G G G C A C A A T T G C A G C T G A T G A C G A
SEQ. ID. NO. 19 A T G A G C T C A A G C T C A T C C A C C A C G A
SEQ. ID. NO. 20 T G G A G G A A C G A G T G A A G G A G G C T G G
SEQ. ID. NO. 21 C T G A G G T G C G G A A T G A C C T G A C T G G

SEQ. ID. NO. 18 C T A T G G G C G G C C G G G G A T T G A G A A A
SEQ. ID. NO. 19 C A G C A A G T G T G A T C C A G G C C A A G C C
SEQ. ID. NO. 20 A A T T G A G A T T A C T T T C C G C C A G A G T
SEQ. ID. NO. 21 A G T T C T G T A T G G C G A G G A C A T T G A G

SEQ. ID. NO. 18 T T C C G A G A G G A A G C T G A G G A A A G G G
SEQ. ID. NO. 19 A C C A A G T A C C T A T A T G A G C T G C T C T
SEQ. ID. NO. 20 T T C T T C T C A G A T C C A G C T G T G C C C G
SEQ. ID. NO. 21 A T T T C A G A C A C C G A G A G C T T C T C C A

SEQ. ID. NO. 18 A T A T C T G C A T C G A C T T C A G T G A A C T
SEQ. ID. NO. 19 A C A A C G A C C C T A T C A A G A T C A T C C T
SEQ. ID. NO. 20 T C A A A A A C C T G A A G C G C C A G G A T G C
SEQ. ID. NO. 21 A C G A T C C C T G T A C C A G T G T C A A A A A

SEQ. ID. NO. 18 C A T C T C C C A G T A C T C T G A T G A G G A A
SEQ. ID. NO. 19 T A T G C C T G G C T G C A G C T C T G T C T C C
SEQ. ID. NO. 20 C C G A A T C A T C G T G G G A C T T T T C T A T
SEQ. ID. NO. 21 G C T G A A G G G G A A T G A T G T G C G G A T C

SEQ. ID. NO. 18 G A G A T C C A G C A T G T G G T A G A G G T G A
SEQ. ID. NO. 19 A C G C T G G T G G C T G A G G C T G C T A G G A
SEQ. ID. NO. 20 G A G A C T G A A G C C C G G A A A G T T T T T T
SEQ. ID. NO. 21 A T C C T T G G C C A G T T T G A C C A G A A T A

SEQ. ID. NO. 18 T T C A A A A T T C C A C G G C C A A A G T C A T
SEQ. ID. NO. 19 T G T G G A A C C T C A T T G T G C T T T C C T A
SEQ. ID. NO. 20 G T G A G G T G T A C A A G G A G C G T C T C T T
SEQ. ID. NO. 21 T G G C A G C A A A A G T G T T C T G T T G T G C

Figure 5d

SEQ. ID. NO. 18 C G T G G T T T T C T C C A G T G G C C C A G A T
SEQ. ID. NO. 19 T G G C T C C A G C T C A C C A G C C C T G T C A
SEQ. ID. NO. 20 T G G G A A G A A G T A C G T C T G G T T C C T C
SEQ. ID. NO. 21 A T A C G A G G A G A A C A T G T A T G G T A G T

SEQ. ID. NO. 18 C T T G A G C C C C T C A T C A A G G A G A T T G
SEQ. ID. NO. 19 A A C C G G C A G C G T T T C C C C A C T T T C T
SEQ. ID. NO. 20 A T T G G G T G G T A T G C T G A C A A T T G G T
SEQ. ID. NO. 21 A A A T A T C A G T G G A T C A T T C C G G G C T

SEQ. ID. NO. 18 T C C G G C G C A A T A T C A C G G G C A A G A T
SEQ. ID. NO. 19 T C C G A A C G C A C C C A T C A G C C A C A C T
SEQ. ID. NO. 20 T C A A G A T C T A C G A C C C T T C T A T C A A
SEQ. ID. NO. 21 G G T A C G A G C C T T C T T G G T G G G A G C A

SEQ. ID. NO. 18 C T G G C T G G C C A G C G A G G C C T G G G C C
SEQ. ID. NO. 19 C C A C A A C C C T A C C C G C G T G A A A C T C
SEQ. ID. NO. 20 C T G C A C A G T G G A T G A G A T G A C T G A G
SEQ. ID. NO. 21 G G T G C A C A C G G A A G C C A A C T C A T C C

SEQ. ID. NO. 18 A G C T C C T C C C T G A T C G C C A T G C C T C
SEQ. ID. NO. 19 T T T G A A A A G T G G G G C T G G A A G A A G A
SEQ. ID. NO. 20 G C G G T G G A G G G C C A C A T C A C A A C T G
SEQ. ID. NO. 21 C G C T G C C T C C G G A A G A A T C T G C T T G

SEQ. ID. NO. 18 A G T A C T T C C A C G T G G T T G G C G G C A C
SEQ. ID. NO. 19 T T G C T A C C A T C C A G C A G A C C A C T G A
SEQ. ID. NO. 20 A G A T T G T C A T G C T G A A T C C T G C C A A
SEQ. ID. NO. 21 C T G C C A T G G A G G G C T A C A T T G G C G T

SEQ. ID. NO. 18 C A T T G G A T T C G C T C T G A A G G C T G G G
SEQ. ID. NO. 19 G G T C T T C A C T T C G A C T C T G G A C G A C
SEQ. ID. NO. 20 T A C C C G C A G C A T T T C C A A C A T G A C A
SEQ. ID. NO. 21 G G A T T T C G A G C C C C T G A G C T C C A A G

SEQ. ID. NO. 18 C A G A T C C C A G G C T T C C G G G A A T T C C
SEQ. ID. NO. 19 C T G G A G G A A C G A G T G A A G G A G G C T G
SEQ. ID. NO. 20 T C C C A G G A A T T T G T G G A G A A A C T A A
SEQ. ID. NO. 21 C A G A T C A A G A C C A T C T C A G G A A A G A

Figure 5e

SEQ. ID. NO. 18 T G A A G A A G G T C C A T C C C A G G A A G T C
SEQ. ID. NO. 19 G A A T T G A G A T T A C T T T C C G C C A G A G
SEQ. ID. NO. 20 C C A A G C G A C T G A A A A G A C A C C C T G A
SEQ. ID. NO. 21 C T C C A C A G C A G T A T G A G A G A G A G T A

SEQ. ID. NO. 18 T G T C C A C A A T G G T T T T G C C A A G G A G
SEQ. ID. NO. 19 T T T C T T C T C A G A T C C A G C T G T G C C C
SEQ. ID. NO. 20 G G A G A C A G G A G G C T T C C A G G A G G C A
SEQ. ID. NO. 21 C A A C A A C A A G C G G T C A G G C G T G G G G

SEQ. ID. NO. 18 T T T T G G G A A G A A A C A T T T A A C T G C C
SEQ. ID. NO. 19 G T C A A A A A C C T G A A G C G C C A G G A T G
SEQ. ID. NO. 20 C C G C T G G C C T A T G A T G C C A T C T G G G
SEQ. ID. NO. 21 C C C A G C A A G T T C C A C G G G T A C G C C T

SEQ. ID. NO. 18 A C C T C C A A G A A G G T G C A A A A G G A C C
SEQ. ID. NO. 19 C C C G A A T C A T C G T G G G A C T T T T C T A
SEQ. ID. NO. 20 C C T T G G C A C T G G C C C T G A A C A A G A C
SEQ. ID. NO. 21 A C G A T G G C A T C T G G G T C A T C G C C A A

SEQ. ID. NO. 18 T T T A C C T G T G G A C A C C T T T C T G A G A
SEQ. ID. NO. 19 T G A G A C T G A A G C C C G G A A A G T T T T T
SEQ. ID. NO. 20 A T C T G G A G G A G G C G G C C G T T C T G G T
SEQ. ID. NO. 21 G A C A C T G C A G A G G G C C A T G G A G A C A

SEQ. ID. NO. 18 G G T C A C G A A G A A A G T G G C G A C A G G T
SEQ. ID. NO. 19 T G T G A G G T G T A C A A G G A G C G T C T C T
SEQ. ID. NO. 20 G T G C G C C T G G A G G A C T T C A A C T A C A
SEQ. ID. NO. 21 C T G C A T G C C A G C A G C C G G C A C C A G C

SEQ. ID. NO. 18 T T A G C A A C A G C T C G A C A G C C T T C C G
SEQ. ID. NO. 19 T T G G G A A G A A G T A C G T C T G G T T C C T
SEQ. ID. NO. 20 A C A A C C A G A C C A T T A C C G A C C A A A T
SEQ. ID. NO. 21 G G A T C C A G G A C T T C A A C T A C A C G G A

SEQ. ID. NO. 18 A C C C C T C T G T A C A G G G G A T G A G A A C
SEQ. ID. NO. 19 C A T T G G G T G G T A T G C T G A C A A T T G G
SEQ. ID. NO. 20 C T A C C G G G C A A T G A A C T C T T C G T C C
SEQ. ID. NO. 21 C C A C A C G C T G G G C A G G A T C A T C C T C

Figure 5f

SEQ. ID. NO. 18 A T C A G C A G T G T C G A G A C C C C T T A C A
SEQ. ID. NO. 19 T T C A A G A T C T A C G A C C C T T C T A T C A
SEQ. ID. NO. 20 T T T G A G G G T G T C T C T G G C C A T G T G G
SEQ. ID. NO. 21 A A T G C C A T G A A C G A G A C C A A C T T C T

SEQ. ID. NO. 18 T A G A T T A C A C G C A T T T A C G G A T A T C
SEQ. ID. NO. 19 A C T G C A C A G T G G A T G A G A T G A C T G A
SEQ. ID. NO. 20 T G T T T G A T G C C A G C G G C T C T C G G A T
SEQ. ID. NO. 21 T C G G G G T C A C G G G T C A A G T T G T A T T

SEQ. ID. NO. 18 C T A C A A T G T G T A C T T A G C A G T C T A C
SEQ. ID. NO. 19 G G C G G T G G A G G G C C A C A T C A C A A C T
SEQ. ID. NO. 20 G G C A T G G A C G C T T A T C G A G C A G C T T
SEQ. ID. NO. 21 C C G G A A T G G G G A G A G A A T G G G G A C C

SEQ. ID. NO. 18 T C C A T T G C C C A C G C C T T G C A A G A T A
SEQ. ID. NO. 19 G A G A T T G T C A T G C T G A A T C C T G C C A
SEQ. ID. NO. 20 C A G G G T G G C A G C T A C A A G A A G A T T G
SEQ. ID. NO. 21 A T T A A A T T T A C T C A A T T T C A A G A C A

SEQ. ID. NO. 18 T A T A T A C C T G C T T A C C T G G G A G A G G
SEQ. ID. NO. 19 A T A C C C G C A G C A T T T C C A A C A T G A C
SEQ. ID. NO. 20 G C T A C T A T G A C A G C A C C A A G G A T G A
SEQ. ID. NO. 21 G C A G G G A G G T G A A G G T G G G A G A G T A

SEQ. ID. NO. 18 G C T C T T C A C C A A T G G C T C C T G T G C A
SEQ. ID. NO. 19 A T C C C A G G A A T T T G T G G A G A A A C T A
SEQ. ID. NO. 20 T C T T T C C T G G T C C A A A A C A G A T A A A
SEQ. ID. NO. 21 C A A C G C T G T G G C C G A C A C A C T G G A G

SEQ. ID. NO. 18 G A C A T C A A G A A A G T T G A G G C G T G G C
SEQ. ID. NO. 19 A C C A A G C G A C T G A A A A G A C A C C C T G
SEQ. ID. NO. 20 T G G A T T G G A G G G T C C C C C C C A G C T G
SEQ. ID. NO. 21 A T C A T C A A T G A C A C C A T C A G G T T C C

SEQ. ID. NO. 18 A G G T C C T G A A G C A C C T A C G G C A T C T
SEQ. ID. NO. 19 A G G A G A C A G G A G G C T T C C A G G A G G C
SEQ. ID. NO. 20 A C C A G A C C C T G G T C A T C A A G A C A T T
SEQ. ID. NO. 21 A A G G A T C C G A A C C A C C A A A A G A C A A

Figure 5g

SEQ. ID. NO. 18 A A A C T T T A C A A A C A A T A T G G G G G A G
SEQ. ID. NO. 19 A C C G C T G G C C T A T G A T G C C A T C T G G
SEQ. ID. NO. 20 C C G C T T C C T G T C A C A G A A A C T C T T T
SEQ. ID. NO. 21 G A C C A T C A T C C T G G A G C A G C T G C G G

SEQ. ID. NO. 18 C A G G T G A C C T T T G A T G A G T G T G G T G
SEQ. ID. NO. 19 G C C T T G G C A C T G G C C C T G A A C A A G A
SEQ. ID. NO. 20 A T C T C C G T C T C A G T T C T C T C C A G C C
SEQ. ID. NO. 21 A A G A T C T C C C T A C C T C T C T A C A G C A

SEQ. ID. NO. 18 A C C T G G T G G G G A A C T A T T C C A T C A T
SEQ. ID. NO. 19 C A T C T G G A G G A G G C G G C C G T T C T G G
SEQ. ID. NO. 20 T G G G C A T T G T C C T A G C T G T T G T C T G
SEQ. ID. NO. 21 T C C T C T C T G C C C T C A C C A T C C T C G G

SEQ. ID. NO. 18 C A A C T G G C A C C T C T C C C C A G A G G A T
SEQ. ID. NO. 19 T G T G C G C C T G G A G G A C T T C A A C T A C
SEQ. ID. NO. 20 T C T G T C C T T T A A C A T C T A C A A C T C A
SEQ. ID. NO. 21 G A T G A T C A T G G C C A G T G C T T T T C T C

SEQ. ID. NO. 18 G G C T C C A T C G T G T T T A A G G A A G T C G
SEQ. ID. NO. 19 A A C A A C C A G A C C A T T A C C G A C C A A A
SEQ. ID. NO. 20 C A T G T C C G T T A T A T C C A G A A C T C A C
SEQ. ID. NO. 21 T T C T T C A A C A T C A A G A A C C G G A A T C

SEQ. ID. NO. 18 G G T A T T A C A A C G T C T A T G C C A A G A A
SEQ. ID. NO. 19 T C T A C C G G G C A A T G A A C T C T T C G T C
SEQ. ID. NO. 20 A G C C C A A C C T G A A C A A C C T G A C T G C
SEQ. ID. NO. 21 A G A A G C T C A T A A A G A T G T C G A G T C C

SEQ. ID. NO. 18 G G G A G A A A G A C T C T T C A T C A A C G A G
SEQ. ID. NO. 19 C T T T G A G G G T G T C T C T G G C C A T G T G
SEQ. ID. NO. 20 T G T G G G C T G C T C A C T G G C T T T A G C T
SEQ. ID. NO. 21 A T A C A T G A A C A A C C T T A T C A T C C T T

SEQ. ID. NO. 18 G A G A A A A T C C T G T G G A G T G G G T T C T
SEQ. ID. NO. 19 G T G T T T G A T G C C A G C G G C T C T C G G A
SEQ. ID. NO. 20 G C T G T C T T C C C C C T G G G G C T C G A T G
SEQ. ID. NO. 21 G G A G G G A T G C T C T C C T A T G C T T C C A

Figure 5h

SEQ. ID. NO. 18 C C A G G G A G G T G C C C T T C T C C A A C T G
SEQ. ID. NO. 19 T G G C A T G G A C G C T T A T C G A G C A G C T
SEQ. ID. NO. 20 G T T A C C A C A T T G G G A G G A A C C A G T T
SEQ. ID. NO. 21 T A T T T C T C T T T G G C C T T G A T G G A T C

SEQ. ID. NO. 18 C A G C C G A G A C T G C C T G G C A G G G A C C
SEQ. ID. NO. 19 T C A G G G T G G C A G C T A C A A G A A G A T T
SEQ. ID. NO. 20 T C C T T T C G T C T G C C A G G C C C G C C T C
SEQ. ID. NO. 21 C T T T G T C T C T G A A A A G A C C T T T G A A

SEQ. ID. NO. 18 A G G A A A G G G A T C A T T G A G G G G G A G C
SEQ. ID. NO. 19 G G C T A C T A T G A C A G C A C C A A G G A T G
SEQ. ID. NO. 20 T G G C T C C T G G G C C T G G G C T T T A G T C
SEQ. ID. NO. 21 A C A C T T T G C A C C G T C A G G A C C T G G A

SEQ. ID. NO. 18 C C A C C T G C T G C T T T G A G T G T G T G G A
SEQ. ID. NO. 19 A T C T T T C C T G G T C C A A A A C A G A T A A
SEQ. ID. NO. 20 T G G G C T A C G G T T C C A T G T T C A C C A A
SEQ. ID. NO. 21 T T C T C A C C G T G G G C T A C A C G A C C G C

SEQ. ID. NO. 18 G T G T C C T G A T G G G G A G T A T A G T G A T
SEQ. ID. NO. 19 A T G G A T T G G A G G G T C C C C C C C A G C T
SEQ. ID. NO. 20 G A T T T G G T G G G T C C A C A C G G T C T T C
SEQ. ID. NO. 21 T T T T G G G G C C A T G T T T G C A A A G A C C

SEQ. ID. NO. 18 G A G A C A G A T G C C A G T G C C T G T A A C A
SEQ. ID. NO. 19 G A C C A G A C C C T G G T C A T C A A G A C A T
SEQ. ID. NO. 20 A C A A A G A A G G A A G A A A A G A A G G A G T
SEQ. ID. NO. 21 T G G A G A G T C C A C G C C A T C T T C A A A A

SEQ. ID. NO. 18 A G T G C C C A G A T G A C T T C T G G T C C A A
SEQ. ID. NO. 19 T C C G C T T C C T G T C A C A G A A A C T C T T
SEQ. ID. NO. 20 G G A G G A A G A C T C T G G A A C C C T G G A A
SEQ. ID. NO. 21 A T G T G A A A A T G A A G A A G A A G A T C A T

SEQ. ID. NO. 18 T G A G A A C C A C A C C T C C T G C A T T G C C
SEQ. ID. NO. 19 T A T C T C C G T C T C A G T T C T C T C C A G C
SEQ. ID. NO. 20 G C T G T A T G C C A C A G T G G G C C T G C T G
SEQ. ID. NO. 21 C A A G G A C C A G A A A C T G C T T G T G A T C

Figure 5i

SEQ. ID. NO. 18 A A G G A G A T C G A G T T T C T G T C G T G G A
SEQ. ID. NO. 19 C T G G G C A T T G T C C T A G C T G T T G T C T
SEQ. ID. NO. 20 G T G G G C A T G G A T G T C C T C A C T C T C G
SEQ. ID. NO. 21 G T G G G G G G C A T G C T G C T G A T C G A C C

SEQ. ID. NO. 18 C G G A G C C C T T T G G G A T C G C A C T C A C
SEQ. ID. NO. 19 G T C T G T C C T T T A A C A T C T A C A A C T C
SEQ. ID. NO. 20 C C A T C T G G C A G A T C G T G G A C C C T C T
SEQ. ID. NO. 21 T G T G T A T C C T G A T C T G C T G G C A G G C

SEQ. ID. NO. 18 C C T C T T T G C C G T G C T G G G C A T T T T C
SEQ. ID. NO. 19 A C A T G T C C G T T A T A T C C A G A A C T C A
SEQ. ID. NO. 20 G C A C C G G A C C A T T G A G A C A T T T G C C
SEQ. ID. NO. 21 T G T G G A C C C C C T G C G A A G G A C A G T G

SEQ. ID. NO. 18 C T G A C A G C C T T T G T G C T G G G T G T G T
SEQ. ID. NO. 19 C A G C C C A A C C T G A A C A A C C T G A C T G
SEQ. ID. NO. 20 A A G G A G G A A C C T A A G G A A G A T A T T G
SEQ. ID. NO. 21 G A G A A G T A C A G C A T G G A G C C G G A C C

SEQ. ID. NO. 18 T T A T C A A G T T C C G C A A C A C A C C C A T
SEQ. ID. NO. 19 C T G T G G G C T G C T C A C T G G C T T T A G C
SEQ. ID. NO. 20 A C G T C T C T A T T C T G C C C C A G C T G G A
SEQ. ID. NO. 21 C A G C A G G A C G G G A T A T C T C C A T C C G

SEQ. ID. NO. 18 T G T C A A G G C C A C C A A C C G A G A G C T C
SEQ. ID. NO. 19 T G C T G T C T T C C C C C T G G G G C T C G A T
SEQ. ID. NO. 20 G C A T T G C A G C T C C A G G A A G A T G A A T
SEQ. ID. NO. 21 C C C T C T C C T G G A G C A C T G T G A G A A C

SEQ. ID. NO. 18 T C C T A C C T C C T C C T C T T C T C C C T G C
SEQ. ID. NO. 19 G G T T A C C A C A T T G G G A G G A A C C A G T
SEQ. ID. NO. 20 A C A T G G C T T G G C A T T T T C T A T G G T T
SEQ. ID. NO. 21 A C C C A T A T G A C C A T C T G G C T T G G C A

SEQ. ID. NO. 18 T C T G C T G C T T C T C C A G C T C C C T G T T
SEQ. ID. NO. 19 T T C C T T T C G T C T G C C A G G C C C G C C T
SEQ. ID. NO. 20 A C A A G G G G C T G C T G C T G C T G C T G G G
SEQ. ID. NO. 21 T C G T C T A T G C C T A C A A G G G A C T T C T

Figure 5J

SEQ. ID. NO. 18	C T T C A T C G G G G A G C C C C A G G A C T G G
SEQ. ID. NO. 19	C T G G C T C C T G G G C C T G G G C T T T A G T
SEQ. ID. NO. 20	A A T C T T C C T T G C T T A T G A G A C C A A G
SEQ. ID. NO. 21	C A T G T T G T T C G G T T G T T T C T T A G C T

SEQ. ID. NO. 18	A C G T G C C G C C T G C G C C A G C C G G C C T
SEQ. ID. NO. 19	C T G G G C T A C G G T T C C A T G T T C A C C A
SEQ. ID. NO. 20	A G T G T G T C C A C T G A G A A G A T C A A T G
SEQ. ID. NO. 21	T G G G A G A C C C G C A A C G T C A G C A T C C

SEQ. ID. NO. 18	T T G G C A T C A G C T T C G T G C T C T G C A T
SEQ. ID. NO. 19	A G A T T T G G T G G G T C C A C A C G G T C T T
SEQ. ID. NO. 20	A T C A C C G G G C T G T G G G C A T G G C T A T
SEQ. ID. NO. 21	C C G C A C T C A A C G A C A G C A A G T A C A T

SEQ. ID. NO. 18	C T C A T G C A T C C T G G T G A A A A C C A A C
SEQ. ID. NO. 19	C A C A A A G A A G G A A G A A A A G A A G G A G
SEQ. ID. NO. 20	C T A C A A T G T G G C A G T C C T G T G C C T C
SEQ. ID. NO. 21	C G G G A T G A G T G T C T A C A A C G T G G G G

SEQ. ID. NO. 18	C G T G T C C T C C T G G T G T T T G A G G C C A
SEQ. ID. NO. 19	T G G A G G A A G A C T C T G G A A C C C T G G A
SEQ. ID. NO. 20	A T C A C T G C T C C T G T C A C C A T G A T T C
SEQ. ID. NO. 21	A T C A T G T G C A T C A T C G G G G C C G C T G

SEQ. ID. NO. 18	A G A T C C C C A C C A G C T T C C A C C G C A A
SEQ. ID. NO. 19	A G C T G T A T G C C A C A G T G G G C C T G C T
SEQ. ID. NO. 20	T G T C C A G C C A G C A G G A T G C A G C C T T
SEQ. ID. NO. 21	T C T C C T T C C T G A C C C G G G A C C A G C C

SEQ. ID. NO. 18	G T G G T G G G G G C T C A A C C T G C A G T T C
SEQ. ID. NO. 19	G G T G G G C A T G G A T G T C C T C A C T C T C
SEQ. ID. NO. 20	T G C C T T T G C C T C T C T T G C C A T A G T T
SEQ. ID. NO. 21	C A A T G T G C A G T T C T G C A T C G T G G C T

SEQ. ID. NO. 18	C T G C T G G T T T T C C T C T G C A C C T T C A
SEQ. ID. NO. 19	G C C A T C T G G C A G A T C G T G G A C C C T C
SEQ. ID. NO. 20	T T C T C C T C C T A T A T C A C T C T T G T T G
SEQ. ID. NO. 21	C T G G T C A T C A T C T T C T G C A G C A C C A

Figure 5k

SEQ. ID. NO. 18 T G C A G A T T G T C A T C T G T G T G A T C T G
SEQ. ID. NO. 19 T G C A C C G G A C C A T T G A G A C A T T T G C
SEQ. ID. NO. 20 T G C T C T T T G T G C C C A A G A T G C G C A G
SEQ. ID. NO. 21 T C A C C C T C T G C C T G G T A T T C G T G C C

SEQ. ID. NO. 18 G C T C T A C A C C G C G C C C C C C T C A A G C
SEQ. ID. NO. 19 C A A G G A G G A A C C T A A G G A A G A T A T T
SEQ. ID. NO. 20 G C T G A T C A C C C G A G G G G A A T G G C A G
SEQ. ID. NO. 21 G A A G C T C A T C A C C C T G A G A A C A A A C

SEQ. ID. NO. 18 T A C C G C A A C C A G G A G C T G G A G G A T G
SEQ. ID. NO. 19 G A C G T C T C T A T T C T G C C C C A G C T G G
SEQ. ID. NO. 20 T C G G A G G C G C A G G A C A C C A T G A A G A
SEQ. ID. NO. 21 C C A G A T G C A G C A A C G C A G A A C A G G C

SEQ. ID. NO. 18 A G A T C A T C T T C A T C A C G T G C C A C G A
SEQ. ID. NO. 19 A G C A T T G C A G C T C C A G G A A G A T G A A
SEQ. ID. NO. 20 C A G G G T C A T C G A C C A A C A A C A A C G A
SEQ. ID. NO. 21 G A T T C C A G T T C A C T C A G A A T C A G A A

SEQ. ID. NO. 18 G G G C T C C C T C A T G G C C C T G G G C T T C
SEQ. ID. NO. 19 T A C A T G G C T T G G C A T T T T C T A T G G T
SEQ. ID. NO. 20 G G A G G A G A A G T C C C G G C T G T T G G A G
SEQ. ID. NO. 21 G A A A G A A G A T T C T A A A A C G T C C A C C

SEQ. ID. NO. 18 C T G A T C G G C T A C A C C T G C C T G C T G G
SEQ. ID. NO. 19 T A C A A G G G G C T G C T G C T G C T G C T G G
SEQ. ID. NO. 20 A A G G A G A A C C G T G A A C T G G A A A A G A
SEQ. ID. NO. 21 T C G G T C A C C A G T G T G A A C C A A G C C A

SEQ. ID. NO. 18 C T G C C A T C T G C T T C T T C T T T G C C T T
SEQ. ID. NO. 19 G A A T C T T C C T T G C T T A T G A G A C C A A
SEQ. ID. NO. 20 T C A T T G C T G A G A A A G A G G A G C G T G T
SEQ. ID. NO. 21 G C A C A T C C C G C C T G G A G G G C C T A C A

SEQ. ID. NO. 18 C A A G T C C C G G A A G C T G C C G G A G A A C
SEQ. ID. NO. 19 G A G T G T G T C C A C T G A G A A G A T C A A T
SEQ. ID. NO. 20 C T C T G A A C T G C G C C A T C A A C T C C A G
SEQ. ID. NO. 21 G T C A G A A A A C C A T C G C C T G C G A A T G

Figure 51

SEQ. ID. NO. 18 T T C A A T G A A G C C A A G T T C A T C A C C T
SEQ. ID. NO. 19 G A T C A C C G G G C T G T G G G C A T G G C T A
SEQ. ID. NO. 20 T C T C G G C A G C A G C T C C G C T C C C G G C
SEQ. ID. NO. 21 A A G A T C A C A G A G C T G G A T A A A G A C T

SEQ. ID. NO. 18 T C A G C A T G C T C A T C T T C T T C A T C G T
SEQ. ID. NO. 19 T C T A C A A T G T G G C A G T C C T G T G C C T
SEQ. ID. NO. 20 G C C A C C C A C C G A C A C C C C C A G A A C C
SEQ. ID. NO. 21 T G G A A G A G G T C A C C A T G C A G C T G C A

SEQ. ID. NO. 18 C T G G A T C T C C T T C A T T C C A G C C T A T
SEQ. ID. NO. 19 C A T C A C T G C T C C T G T C A C C A T G A T T
SEQ. ID. NO. 20 C T C T G G G G G C C T G C C C A G G G G A C C C
SEQ. ID. NO. 21 G G A C A C A C C A G A A A A G A C C A C C T A C

SEQ. ID. NO. 18 G C C A G C A C C T A T G G C A A G T T T G T C T
SEQ. ID. NO. 19 C T G T C C A G C C A G C A G G A T G C A G C C T
SEQ. ID. NO. 20 C C T G A G C C C C C C G A C C G G C T T A G C T
SEQ. ID. NO. 21 A T T A A A C A G A A C C A C T A C C A A G A G C

SEQ. ID. NO. 18 C T G C C G T A G A G G T G A T T G C C A T C C T
SEQ. ID. NO. 19 T T G C C T T T G C C T C T C T T G C C A T A G T
SEQ. ID. NO. 20 G T G A T G G G A G T C G A G T G C A T T T G C T
SEQ. ID. NO. 21 T C A A T G A C A T C C T C A A C C T G G G A A A

SEQ. ID. NO. 18 G G C A G C C A G C T T T G G C T T G C T G G C G
SEQ. ID. NO. 19 T T T C T C C T C C T A T A T C A C T C T T G T T
SEQ. ID. NO. 20 T T A T A A G T G A G G G T A G G G T G A G G G A
SEQ. ID. NO. 21 C T T C A C T G A G A G C A C A G A T G G A G G A

SEQ. ID. NO. 18 T G C A T C T T C T T C A A C A A G A T C T A C A
SEQ. ID. NO. 19 G T G C T C T T T G T G C C C A A G A T G C G C A
SEQ. ID. NO. 20 G G A C A G G C C A G T A G G G G G A G G G A A A
SEQ. ID. NO. 21 A A G G C C A T T T T A A A A A A T C A C C T C G

SEQ. ID. NO. 18 T C A T T C T C T T C A A G C C A T C C C G C A A
SEQ. ID. NO. 19 G G C T G A T C A C C C G A G G G G A A T G G C A
SEQ. ID. NO. 20 G G G A G A G G G G A A G G G C A G G G G A C T C
SEQ. ID. NO. 21 A T C A A A A T C C C C A G C T A C A G T G G A A

Figure 5m

SEQ. ID. NO. 18 C A C C A T C G A G G A G G T G C G T T G C A G C
SEQ. ID. NO. 19 G T C G G A G G C G C A G G A C A C C A T G A A G
SEQ. ID. NO. 20 A G G A A G C A G G G G G T C C C C A T C C C C A
SEQ. ID. NO. 21 C A C A A C A G A G C C C T C T C G A A C A T G C

SEQ. ID. NO. 18 A C C G C A G C T C A C G C T T T C A A G G T G G
SEQ. ID. NO. 19 A C A G G G T C A T C G A C C A A C A A C A A C G
SEQ. ID. NO. 20 G C T G G G A A G A A C A T G C T A T C C A A T C
SEQ. ID. NO. 21 A A A G A T C C T A T A G A A G A T A T A A A C T

SEQ. ID. NO. 18 C T G C C C G G G C C A C G C T G C G C C G C A G
SEQ. ID. NO. 19 A G G A G G A G A A G T C C C G G C T G T T G G A
SEQ. ID. NO. 20 T C A T C T C T T G T A A A T A C A T G T C C C C
SEQ. ID. NO. 21 C T C C A G A A C A C A T C C A G C G T C G G C T

SEQ. ID. NO. 18 C A A C G T C T C C C G C A A G C G G T C C A G C
SEQ. ID. NO. 19 G A A G G A G A A C C G T G A A C T G G A A A A G
SEQ. ID. NO. 20 C T G T G A G T T C T G G G C T G A T T T G G G T
SEQ. ID. NO. 21 G T C C C T C C A G C T C C C C A T C C T C C A C

SEQ. ID. NO. 18 A G C C T T G G A G G C T C C A C G G G A T C C A
SEQ. ID. NO. 19 A T C A T T G C T G A G A A A G A G G A G C G T G
SEQ. ID. NO. 20 C T C T C A T A C C T C T G G G A A A C A G A C C
SEQ. ID. NO. 21 C A C G C C T A C C T C C C A T C C A T C G G A G

SEQ. ID. NO. 18 C C C C C T C C T C C T C C A T C A G C A G C A A
SEQ. ID. NO. 19 T C T C T G A A C T G C G C C A T C A G C T C C A
SEQ. ID. NO. 20 T T T T T C T C T C T T A C T G C T T C A T G T A
SEQ. ID. NO. 21 G C G T G G A C G C C A G C T G T G T C A G C C C

SEQ. ID. NO. 18 G A G C A A C A G C G A A G A C C C A T T C C C A
SEQ. ID. NO. 19 G T C T C G G C A G C A G C T C C G C T C C C G G
SEQ. ID. NO. 20 A T T T T G T A T C A C C T C T T C A C A A T T T
SEQ. ID. NO. 21 C T G C G T C A G C C C C A C C G C C A G C C C C

SEQ. ID. NO. 18 C A G C C C G A G A G G C A G A A G C A G C A G C
SEQ. ID. NO. 19 C G C C A C C C A C C G A C A C C C C C A G A A C
SEQ. ID. NO. 20 A G T T C G T A C C T G G C T T G A A G C T G C T
SEQ. ID. NO. 21 C G C C A C A G A C A T G T G C C A C C C T C C T

Figure 5n

SEQ. ID. NO. 18 A G C C G C T G G C C C T A A C C C A G C A A G A
SEQ. ID. NO. 19 C C T C T G G G G G C C T G C C C A G G G G A C C
SEQ. ID. NO. 20 C A C T G C T C A C A C G C T G C C T C C T C A G
SEQ. ID. NO. 21 T C C G A G T C A T G G T C T C G G G C C T G T A

SEQ. ID. NO. 18 G C A G C A G C A G C A G C C C C T G A C C C T C
SEQ. ID. NO. 19 C C C T G A G C C C C C C G A C C G G C T T A G C
SEQ. ID. NO. 20 C A G C C T C A C T G C A T C T T T C T C T T C C
SEQ. ID. NO. 21 A G G G T G G G A G G C C T G G G C C C G G G G C

SEQ. ID. NO. 18 C C A C A G C A G C A A C G A T C T C A G C A G C
SEQ. ID. NO. 19 T G T G A T G G G A G T C G A G T G C A T T T G C
SEQ. ID. NO. 20 C A T G C A A C A C C C T C T T C T A G T T A C C
SEQ. ID. NO. 21 C T C C C C C G T G A C A G A A C C A C A C T G G

SEQ. ID. NO. 18 A G C C C A G A T G C A A G C A G A A G G T C A T
SEQ. ID. NO. 19 T T T A T A A G T G A G G G T A G G G T G A G G G
SEQ. ID. NO. 20 A C G G C A A C C C C T
SEQ. ID. NO. 21 G C A G A G G G G T C T G C T G C A G A A A C A C

SEQ. ID. NO. 18 C T T T G G C A G C G G C A C G G T C A C C T T C
SEQ. ID. NO. 19 A G G A C A G G C C A G T A G G G G G A G G G A A
SEQ. ID. NO. 20
SEQ. ID. NO. 21 T G T C G G C T C T G G C T G C G G A G A A G C T

SEQ. ID. NO. 18 T C A C T G A G C T T T G A T G A G C C T C A G A
SEQ. ID. NO. 19 A G G G A G A G G G G A A G G G C A G G G G A C T
SEQ. ID. NO. 20
SEQ. ID. NO. 21 G G G C A C C A T G G C T G G C C T C T C A G G A

SEQ. ID. NO. 18 A G A A C G C C A T G G C C C A C G G G A A T T C
SEQ. ID. NO. 19 C A G G A A G C A G G G G G T C C C C A T C C C C
SEQ. ID. NO. 20
SEQ. ID. NO. 21 C C A C T C G G A T G G C A C T C A G G T G G A C

SEQ. ID. NO. 18 T A C G C A C C A G A A C T C C C T G G A G G C C
SEQ. ID. NO. 19 A G C T G G G A A G A A C A T G C T A T C C A A T
SEQ. ID. NO. 20
SEQ. ID. NO. 21 A G G A C G G G G C A G G G G G A G A C T T G G C

Figure 5o

SEQ. ID. NO. 18	C A G A A A A G C A G C G A T A C G C T G A C C C
SEQ. ID. NO. 19	C T C A T C T C T T G T A A A T A C A T G T C C C
SEQ. ID. NO. 20	
SEQ. ID. NO. 21	A C C T G A C C T C G A G C C T T A T T T G T G A
SEQ. ID. NO. 18	G A C A C C A G C C A T T A C T C C C G C T G C A
SEQ. ID. NO. 19	C C T G T G A G T T C T G G G C T G A T T T G G G
SEQ. ID. NO. 20	
SEQ. ID. NO. 21	A G T C C T T A T T T C T T C A C A A A G A A G A
SEQ. ID. NO. 18	G T G C G G G G A A A C G G A C T T A G A T C T G
SEQ. ID. NO. 19	T C T C T C A T A C C T C T G G G A A A C A G A C
SEQ. ID. NO. 20	
SEQ. ID. NO. 21	G G A A C G G A A A T G G G A C G T C T T C C T T
SEQ. ID. NO. 18	A C C G T C C A G G A A A C A G G T C T G C A A G
SEQ. ID. NO. 19	C T T T T T C T C T C T T A C T G C T T C A T G T
SEQ. ID. NO. 20	
SEQ. ID. NO. 21	A A C A T C T G C A A A C A A G G A G G C G C T G
SEQ. ID. NO. 18	G A C C T G T G G G T G G A G A C C A G C G G C C
SEQ. ID. NO. 19	A A T T T T G T A T C A C C T C T T C A C A A T T
SEQ. ID. NO. 20	
SEQ. ID. NO. 21	G G A T A T C A A A C T T G C A A A A A A A A A A
SEQ. ID. NO. 18	A G A G G T G G A G G A C C C T G A A G A G T T G
SEQ. ID. NO. 19	T A G T T C G T A C C T G G C T T G A A G C T G C
SEQ. ID. NO. 20	
SEQ. ID. NO. 21	A A A A A A A A A A A A A
SEQ. ID. NO. 18	T C C C C A G C A C T T G T A G T G T C C A G T T
SEQ. ID. NO. 19	T C A C T G C T C A C A C G C T G C C T C C T C A
SEQ. ID. NO. 20	
SEQ. ID. NO. 21	
SEQ. ID. NO. 18	C A C A G A G C T T T G T C A T C A G T G G T G G
SEQ. ID. NO. 19	G C A G C C T C A C T G C A T C T T T C T C T T C
SEQ. ID. NO. 20	
SEQ. ID. NO. 21	

Figure 5p

SEQ. ID. NO. 18 A G G C A G C A C T G T T A C A G A A A A C G T A
SEQ. ID. NO. 19 C C A T G C A A C A C C C T C T T C T A G T T A C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18 G T G A A T T C A
SEQ. ID. NO. 19 C A C G G C A A C C C C T G C A G C T C C T C T G
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 C C T T T G T G C T C T G T T C C T G T C C A G C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 A G G G G T C T C C C A A C A A G T G C T C T T T
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 C C A C C C C A A A G G G G C C T C T C C T T T T
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 C T C C A C T G T C A T A A T C T C T T T C C A T
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 C T T A C T T G C C C T T C T A T A C T T T C T C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 A C A T G T G G C T C C C C C T G A A T T T T G C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

Figure 5q

SEQ. ID. NO. 18
SEQ. ID. NO. 19 T T C C T T T G G G G A G C T C A T T C T T T C G
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 C C A A G G T C A C A T G C T C C C T T G C C T C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 T G G C T C C G T G C A
SEQ. ID. NO. 20
SEQ. ID. NO. 21

Figure 5r

FIGURE 6a

SEQ. ID. NO. 22	A T G C T G C T G C T G C T G C T G G T G C C T C T C T T C
SEQ. ID. NO. 23	A T G G G C C C G G G G G G A C C C T G T A C C C C A G T G
SEQ. ID. NO. 22	C T C C G C C C C C T G G G C G C T G G C G G G G C G C A G
SEQ. ID. NO. 23	G G G T G G C C G C T G C C T C T T C T G C T G G T G A T G
SEQ. ID. NO. 22	A C C C C C A A C G C C A C C T C G G A A G G T T G C C A G
SEQ. ID. NO. 23	G C G G C T G G G G T G G C T C C G G T G T G G G C C T C T
SEQ. ID. NO. 22	A T T A T A C A T C C G C C C T G G G A A G G T G G C A T C
SEQ. ID. NO. 23	C A C T C C C C T C A T C T C C C G C G G C C T C A C C C G
SEQ. ID. NO. 22	A G G T A C C G T G G C T T G A C T C G C G A C C A G G T G
SEQ. ID. NO. 23	A G G G T C C C C C C G C A C C C C T C C T C A G A A C G G
SEQ. ID. NO. 22	A A G G C C A T C A A C T T C C T G C C T G T G G A C T A T
SEQ. ID. NO. 23	C G T G C A G T A T A C A T C G G G G C G C T G T T T C C C
SEQ. ID. NO. 22	G A G A T C G A A T A T G T G T G C C G A G G G G A G C G C
SEQ. ID. NO. 23	A T G A G C G G G G G C T G G C C G G G G G G C C A G G C C
SEQ. ID. NO. 22	G A G G T G G T G G G G C C C A A G G T G C G C A A A T G C
SEQ. ID. NO. 23	T G C C A G C C C G C G G T G G A G A T G G C G C T G G A G
SEQ. ID. NO. 22	C T G G C C A A C G G C T C C T G G A C G G A T A T G G A C
SEQ. ID. NO. 23	G A C G T T A A C A G C C G C A G A G A C A T C C T G C C G
SEQ. ID. NO. 22	A C A C C C A G C C G C T G T G T C C G A A T C T G C T C C
SEQ. ID. NO. 23	G A C T A C G A G C T C A A G C T T A T C C A C C A C G A C
SEQ. ID. NO. 22	A A G T C T T A T T T G A C C C T G G A A A A T G G G A A G
SEQ. ID. NO. 23	A G C A A G T G T G A C C C A G G G C A A G C C A C C A A G
SEQ. ID. NO. 22	G T T T T C C T G A C G G G T G G G G A C C T C C C A G C T
SEQ. ID. NO. 23	T A C T T G T A C G A A C T A C T C T A C A A T G A C C C C

FIGURE 6b

SEQ. ID. NO. 22 C T G G A T G G A G C C C G G G T G G A G T T C C G A T G T
SEQ. ID. NO. 23 A T C A A G A T C A T T C T C A T G C C T G G C T G T A G T

SEQ. ID. NO. 22 G A C C C C G A C T T C C A T C T G G T G G G C A G C T C C
SEQ. ID. NO. 23 T C T G T C T C C A C A C T T G T A G C T G A G G C T G C C

SEQ. ID. NO. 22 C G G A G C G T C T G T A G T C A G G G C C A G T G G A G C
SEQ. ID. NO. 23 C G G A T G T G G A A C C T T A T T G T G C T C T C A T A T

SEQ. ID. NO. 22 A C C C C C A A G C C C C A C T G C C A G G T G A A T C G A
SEQ. ID. NO. 23 G G C T C C A G T T C A C C A G C C T T G T C A A A C C G A

SEQ. ID. NO. 22 A C G C C A C A C T C A G A A C G G C G T G C A G T A T A C
SEQ. ID. NO. 23 C A G C G G T T T C C C A C G T T C T T C C G G A C G C A T

SEQ. ID. NO. 22 A T C G G G G C G C T G T T T C C C A T G A G C G G G G G C
SEQ. ID. NO. 23 C C A T C C G C C A C A C T C C A C A A T C C C A C C C G G

SEQ. ID. NO. 22 T G G C C G G G G G G C C A G G C C T G C C A G C C C G C G
SEQ. ID. NO. 23 G T G A A A C T C T T C G A A A A G T G G G G C T G G A A G

SEQ. ID. NO. 22 G T G G A G A T G G C G C T G G A G G A C G T T A A C A G C
SEQ. ID. NO. 23 A A G A T C G C T A C C A T C C A A C A G A C C A C C G A G

SEQ. ID. NO. 22 C G C A G A G A C A T C C T G C C G G A C T A C G A G C T C
SEQ. ID. NO. 23 G T C T T C A C C T C A A C G C T G G A T G A C C T G G A G

SEQ. ID. NO. 22 A A G C T T A T C C A C C A C G A C A G C A A G T G T G A C
SEQ. ID. NO. 23 G A G C G A G T G A A A G A G G C T G G G A T C G A G A T C

SEQ. ID. NO. 22 C C A G G G C A A G C C A C C A A G T A C T T G T A C G A A
SEQ. ID. NO. 23 A C T T T C C G A C A G A G T T T C T T C T C G G A T C C A

SEQ. ID. NO. 22 C T A C T C T A C A A T G A C C C C A T C A A G A T C A T T
SEQ. ID. NO. 23 G C T G T G C C T G T T A A A A A C C T G A A G C G T C A A

SEQ. ID. NO. 22 C T C A T G C C T G G C T G T A G T T C T G T C T C C A C A
SEQ. ID. NO. 23 G A T G C T C G A A T C A T C G T G G G A C T T T T C T A T

FIGURE 6c

SEQ. ID. NO. 22 C T T G T A G C T G A G G C T G C C C G G A T G T G G A A C
SEQ. ID. NO. 23 G A G A C G G A A G C C C G G A A A G T T T T T T G T G A G

SEQ. ID. NO. 22 C T T A T T G T G C T C T C A T A T G G C T C C A G T T C A
SEQ. ID. NO. 23 G T C T A T A A G G A A A G G C T C T T T G G G A A G A A G

SEQ. ID. NO. 22 C C A G C C T T G T C A A A C C G A C A G C G G T T T C C C
SEQ. ID. NO. 23 T A C G T C T G G T T C C T C A T C G G G T G G T A T G C T

SEQ. ID. NO. 22 A C G T T C T T C C G G A C G C A T C C A T C C G C C A C A
SEQ. ID. NO. 23 G A C A A C T G G T T C A A G A C C T A T G A C C C G T C A

SEQ. ID. NO. 22 C T C C A C A A T C C C A C C C G G G T G A A A C T C T T C
SEQ. ID. NO. 23 A T C A A T T G T A C A G T G G A A G A A A T G A C C G A G

SEQ. ID. NO. 22 G A A A A G T G G G G C T G G A A G A A G A T C G C T A C C
SEQ. ID. NO. 23 G C G G T G G A G G G C C A C A T C A C C A C G G A G A T T

SEQ. ID. NO. 22 A T C C A A C A G A C C A C C G A G G T C T T C A C C T C A
SEQ. ID. NO. 23 G T C A T G C T G A A C C C T G C C A A C A C C C G A A G C

SEQ. ID. NO. 22 A C G C T G G A T G A C C T G G A G G A G C G A G T G A A A
SEQ. ID. NO. 23 A T T T C C A A C A T G A C G T C A C A G G A A T T T G T G

SEQ. ID. NO. 22 G A G G C T G G G A T C G A G A T C A C T T T C C G A C A G
SEQ. ID. NO. 23 G A G A A A C T A A C C A A G C G G C T G A A A A G A C A C

SEQ. ID. NO. 22 A G T T T C T T C T C G G A T C C A G C T G T G C C T G T T
SEQ. ID. NO. 23 C C C G A G G A G A C T G G A G G C T T C C A G G A G G C A

SEQ. ID. NO. 22 A A A A A C C T G A A G C G T C A A G A T G C T C G A A T C
SEQ. ID. NO. 23 C C A C T G G C C T A T G A T G C T A T C T G G G C C T T G

SEQ. ID. NO. 22 A T C G T G G G A C T T T T C T A T G A G A C G G A A G C C
SEQ. ID. NO. 23 G C T T T G G C C T T G A A C A A G A C G T C T G G A G G A

SEQ. ID. NO. 22 C G G A A A G T T T T T T G T G A G G T C T A T A A G G A A
SEQ. ID. NO. 23 G G T G G T C G T T C C G G C G T G C G C C T G G A G G A C

FIGURE 6d

SEQ. ID. NO. 22 A G G C T C T T T G G G A A G A A G T A C G T C T G G T T C
SEQ. ID. NO. 23 T T T A A C T A C A A C A A C C A G A C C A T T A C A G A C

SEQ. ID. NO. 22 C T C A T C G G G T G G T A T G C T G A C A A C T G G T T C
SEQ. ID. NO. 23 C A G A T C T A C C G G G C C A T G A A C T C C T C C T C C

SEQ. ID. NO. 22 A A G A C C T A T G A C C C G T C A A T C A A T T G T A C A
SEQ. ID. NO. 23 T T T G A G G G C G T T T C T G G C C A T G T G G T C T T T

SEQ. ID. NO. 22 G T G G A A G A A A T G A C C G A G G C G G T G G A G G G C
SEQ. ID. NO. 23 G A T G C C A G C G G C T C C C G G A T G G C A T G G A C A

SEQ. ID. NO. 22 C A C A T C A C C A C G G A G A T T G T C A T G C T G A A C
SEQ. ID. NO. 23 C T T A T C G A G C A G C T A C A G G G C G G C A G C T A C

SEQ. ID. NO. 22 C C T G C C A A C A C C C G A A G C A T T T C C A A C A T G
SEQ. ID. NO. 23 A A G A A G A T C G G C T A C T A C G A C A G C A C C A A G

SEQ. ID. NO. 22 A C G T C A C A G G A A T T T G T G G A G A A A C T A A C C
SEQ. ID. NO. 23 G A T G A T C T T T C C T G G T C C A A A A C G G A C A A G

SEQ. ID. NO. 22 A A G C G G C T G A A A A G A C A C C C C G A G G A G A C T
SEQ. ID. NO. 23 T G G A T T G G A G G G T C T C C C C C A G C T G A C C A G

SEQ. ID. NO. 22 G G A G G C T T C C A G G A G G C A C C A C T G G C C T A T
SEQ. ID. NO. 23 A C C T T G G T C A T C A A G A C A T T C C G T T T C C T G

SEQ. ID. NO. 22 G A T G C T A T C T G G G C C T T G G C T T T G G C C T T G
SEQ. ID. NO. 23 T C T C A G A A A C T C T T T A T C T C C G T C T C A G T T

SEQ. ID. NO. 22 A A C A A G A C G T C T G G A G G A G G T G G T C G T T C C
SEQ. ID. NO. 23 C T C T C C A G C C T G G G C A T T G T T C T T G C T G T T

SEQ. ID. NO. 22 G G C G T G C G C C T G G A G G A C T T T A A C T A C A A C
SEQ. ID. NO. 23 G T C T G T C T G T C C T T T A A C A T C T A C A A C T C C

SEQ. ID. NO. 22 A A C C A G A C C A T T A C A G A C C A G A T C T A C C G G
SEQ. ID. NO. 23 C A C G T T C G T T A T A T C C A G A A C T C C C A G C C C

FIGURE 6e

SEQ. ID. NO. 22 G C C A T G A A C T C C T C C T C C T T T G A G G G C G T T
SEQ. ID. NO. 23 A A C C T G A A C A A T C T G A C T G C T G T G G G C T G C

SEQ. ID. NO. 22 T C T G G C C A T G T G G T C T T T G A T G C C A G C G G C
SEQ. ID. NO. 23 T C A C T G G C A C T G G C T G C T G T C T T C C C T C T C

SEQ. ID. NO. 22 T C C C G G A T G G C A T G G A C A C T T A T C G A G C A G
SEQ. ID. NO. 23 G G G C T G G A T G G T T A C C A C A T A G G G A G A A G C

SEQ. ID. NO. 22 C T A C A G G G C G G C A G C T A C A A G A A G A T C G G C
SEQ. ID. NO. 23 C A G T T C C C G T T T G T C T G C C A G G C C C G C C T T

SEQ. ID. NO. 22 T A C T A C G A C A G C A C C A A G G A T G A T C T T T C C
SEQ. ID. NO. 23 T G G C T C T T G G G C T T G G G C T T T A G T C T G G G C

SEQ. ID. NO. 22 T G G T C C A A A A C G G A C A A G T G G A T T G G A G G G
SEQ. ID. NO. 23 T A T G G C T C T A T G T T C A C C A A G A T C T G G T G G

SEQ. ID. NO. 22 T C T C C C C C A G C T G A C C A G A C C T T G G T C A T C
SEQ. ID. NO. 23 G T C C A C A C A G T C T T C A C G A A G A A G G A G G A G

SEQ. ID. NO. 22 A A G A C A T T C C G T T T C C T G T C T C A G A A A C T C
SEQ. ID. NO. 23 A A G A A G G A G T G G A G G A A G A C C C T A G A G C C C

SEQ. ID. NO. 22 T T T A T C T C C G T C T C A G T T C T C T C C A G C C T G
SEQ. ID. NO. 23 T G G A A A C T C T A T G C C A C T G T G G G C C T G C T G

SEQ. ID. NO. 22 G G C A T T G T T C T T G C T G T T G T C T G T C T G T C C
SEQ. ID. NO. 23 G T G G G C A T G G A T G T C C T G A C T C T T G C C A T C

SEQ. ID. NO. 22 T T T A A C A T C T A C A A C T C C C A C G T T C G T T A T
SEQ. ID. NO. 23 T G G C A G A T T G T G G A C C C C T T G C A C C G A A C C

SEQ. ID. NO. 22 A T C C A G A A C T C C C A G C C C A A C C T G A A C A A T
SEQ. ID. NO. 23 A T T G A G A C T T T T G C C A A G G A G G A A C C A A A G

SEQ. ID. NO. 22 C T G A C T G C T G T G G G C T G C T C A C T G G C A C T G
SEQ. ID. NO. 23 G A A G A C A T C G A T G T C T C C A T T C T G C C C C A G

FIGURE 6f

SEQ. ID. NO. 22 G C T G C T G T C T T C C C T C T C G G G C T G G A T G G T
SEQ. ID. NO. 23 T T G G A G C A C T G C A G C T C C A A G A A G A T G A A T

SEQ. ID. NO. 22 T A C C A C A T A G G G A G A A G C C A G T T C C C G T T T
SEQ. ID. NO. 23 A C G T G G C T T G G C A T T T T C T A T G G T T A C A A G

SEQ. ID. NO. 22 G T C T G C C A G G C C C G C C T T T G G C T C T T G G G C
SEQ. ID. NO. 23 G G G C T G C T G C T G C T G C T G G G A A T C T T T C T T

SEQ. ID. NO. 22 T T G G G C T T T A G T C T G G G C T A T G G C T C T A T G
SEQ. ID. NO. 23 G C T T A C G A A A C C A A G A G C G T G T C C A C T G A A

SEQ. ID. NO. 22 T T C A C C A A G A T C T G G T G G G T C C A C A C A G T C
SEQ. ID. NO. 23 A A G A T C A A T G A C C A C A G G G C C G T G G G C A T G

SEQ. ID. NO. 22 T T C A C G A A G A A G G A G G A G A A G A A G G A G T G G
SEQ. ID. NO. 23 G C T A T C T A C A A T G T C G C G G T C C T G T G T C T C

SEQ. ID. NO. 22 A G G A A G A C C C T A G A G C C C T G G A A A C T C T A T
SEQ. ID. NO. 23 A T C A C T G C T C C T G T G A C C A T G A T C C T T T C C

SEQ. ID. NO. 22 G C C A C T G T G G G C C T G C T G G T G G G C A T G G A T
SEQ. ID. NO. 23 A G T C A G C A G G A C G C A G C C T T T G C C T T T G C C

SEQ. ID. NO. 22 G T C C T G A C T C T T G C C A T C T G G C A G A T T G T G
SEQ. ID. NO. 23 T C T C T G G C C A T C G T G T T C T C T T C C T A C A T C

SEQ. ID. NO. 22 G A C C C C T T G C A C C G A A C C A T T G A G A C T T T T
SEQ. ID. NO. 23 A C T C T G G T T G T G C T C T T T G T G C C C A A G A T G

SEQ. ID. NO. 22 G C C A A G G A G G A A C C A A A G G A A G A C A T C G A T
SEQ. ID. NO. 23 C G C A G G C T G A T C A C C C G A G G G G A A T G G C A G

SEQ. ID. NO. 22 G T C T C C A T T C T G C C C C A G T T G G A G C A C T G C
SEQ. ID. NO. 23 T C T G A A A C G C A G G A C A C C A T G A A A A C A G G A

SEQ. ID. NO. 22 A G C T C C A A G A A G A T G A A T A C G T G G C T T G G C
SEQ. ID. NO. 23 T C A T C C A C C A A C A A C A A C G A G G A A G A G A A G

SEQ. ID. NO. 22 A T T T T C T A T G G T T A C A A G G G G C T G C T G C T G
SEQ. ID. NO. 23 T C C C G A C T G T T G G A G A A G G A A A A C C G A G A A

SEQ. ID. NO. 22 C T G C T G G G A A T C T T T C T T G C T T A C G A A A C C
SEQ. ID. NO. 23 C T G G A A A A G A T C A T C G C T G A G A A A G A G G A G

SEQ. ID. NO. 22 A A G A G C G T G T C C A C T G A A A A G A T C A A T G A C
SEQ. ID. NO. 23 C G C G T C T C T G A A C T G C G C C A T C A G C T C C A G

SEQ. ID. NO. 22 C A C A G G G C C G T G G G C A T G G C T A T C T A C A A T
SEQ. ID. NO. 23 T C T C G G C A G C A A C T C C G C T C A C G G C G C C A C

SEQ. ID. NO. 22 G T C G C G G T C C T G T G T C T C A T C A C T G C T C C T
SEQ. ID. NO. 23 C C C C C A A C A C C C C C A G A T C C C T C T G G G G G C

SEQ. ID. NO. 22 G T G A C C A T G A T C C T T T C C A G T C A G C A G G A C
SEQ. ID. NO. 23 C T T C C C A G G G G A C C C T C T G A G C C C C C T G A C

SEQ. ID. NO. 22 G C A G C C T T T G C C T T T G C C T C T C T G G C C A T C
SEQ. ID. NO. 23 C G G C T T A G C T G T G A T G G G A G T C G A G T A C A T

SEQ. ID. NO. 22 G T G T T C T C T T C C T A C A T C A C T C T G G T T G T G
SEQ. ID. NO. 23 T T G C T T T A C A A G

SEQ. ID. NO. 22 C T C T T T G T G C C C A A G A T G C G C A G G C T G A T C
SEQ. ID. NO. 23

SEQ. ID. NO. 22 A C C C G A G G G G A A T G G C A G T C T G A A A C G C A G
SEQ. ID. NO. 23

SEQ. ID. NO. 22 G A C A C C A T G A A A A C A G G A T C A T C C A C C A A C
SEQ. ID. NO. 23

SEQ. ID. NO. 22 A A C A A C G A G G A A G A G A A G T C C C G A C T G T T G
SEQ. ID. NO. 23

SEQ. ID. NO. 22 G A G A A G G A A A A C C G A G A A C T G G A A A A G A T C
SEQ. ID. NO. 23

FIGURE 6L

SEQ. ID. NO. 22 A T C G C T G A G A A A G A G G A G C G C G T C T C T G A A
SEQ. ID. NO. 23

SEQ. ID. NO. 22 C T G C G C C A T C A G C T C C A G T C T C G G C A G C A A
SEQ. ID. NO. 23

SEQ. ID. NO. 22 C T C C G C T C A C G G C G C C A C C C C C C A A C A C C C
SEQ. ID. NO. 23

SEQ. ID. NO. 22 C C A G A T C C C T C T G G G G G C C T T C C C A G G G G A
SEQ. ID. NO. 23

SEQ. ID. NO. 22 C C C T C T G A G C C C C C T G A C C G G C T T A G C T G T
SEQ. ID. NO. 23

SEQ. ID. NO. 22 G A T G G G A G T C G A G T A C A T T T G C T T T A C A A G
SEQ. ID. NO. 23

FIGURE 7c

SEQ. ID. NO. 24 M L L L L L V P L F L R P L G A G G A Q T P N A T S E G C Q
SEQ. ID. NO. 25 M G P G G P C T P V G W P L P L L L V M A A G V A P V W A S

SEQ. ID. NO. 24 I I H P P W E G G I R Y R G L T R D Q V K A I N F L P V D Y
SEQ. ID. NO. 25 H S P H L P R P H P R V P P H P S S E R R A V Y I G A L F P

SEQ. ID. NO. 24 E I E Y V C R G E R E V V G P K V R K C L A N G S W T D M D
SEQ. ID. NO. 25 M S G G W P G G Q A C Q P A V E M A L E D V N S R R D I L P

SEQ. ID. NO. 24 T P S R C V R I C S K S Y L T L E N G K V F L T G G D L P A
SEQ. ID. NO. 25 D Y E L K L I H H D S K C D P G Q A T K Y L Y E L L Y N D P

SEQ. ID. NO. 24 L D G A R V E F R C D P D F H L V G S S R S V C S Q G Q W S
SEQ. ID. NO. 25 I K I I L M P G C S S V S T L V A E A A R M W N L I V L S Y

SEQ. ID. NO. 24 T P K P H C Q V N R T P H S E R R A V Y I G A L F P M S G G
SEQ. ID. NO. 25 G S S S P A L S N R Q R F P T F F R T H P S A T L H N P T R

SEQ. ID. NO. 24 W P G G Q A C Q P A V E M A L E D V N S R R D I L P D Y E L
SEQ. ID. NO. 25 V K L F E K W G W K K I A T I Q Q T T E V F T S T L D D L E

SEQ. ID. NO. 24 K L I H H D S K C D P G Q A T K Y L Y E L L Y N D P I K I I
SEQ. ID. NO. 25 E R V K E A G I E I T F R Q S F F S D P A V P V K N L K R Q

SEQ. ID. NO. 24 L M P G C S S V S T L V A E A A R M W N L I V L S Y G S S S
SEQ. ID. NO. 25 D A R I I V G L F Y E T E A R K V F C E V Y K E R L F G K K

SEQ. ID. NO. 24 P A L S N R Q R F P T F F R T H P S A T L H N P T R V K L F
SEQ. ID. NO. 25 Y V W F L I G W Y A D N W F K T Y D P S I N C T V E E M T E

SEQ. ID. NO. 24 E K W G W K K I A T I Q Q T T E V F T S T L D D L E E R V K
SEQ. ID. NO. 25 A V E G H I T T E I V M L N P A N T R S I S N M T S Q E F V

SEQ. ID. NO. 24 E A G I E I T F R Q S F F S D P A V P V K N L K R Q D A R I
SEQ. ID. NO. 25 E K L T K R L K R H P E E T G G F Q E A P L A Y D A I W A L

FIGURE 7I

SEQ. ID. NO. 24	I V G L F Y E T E A R K V F C E V Y K E R L F G K K Y V W F
SEQ. ID. NO. 25	A L A L N K T S G G G G R S G V R L E D F N Y N N Q T I T D
SEQ. ID. NO. 24	L I G W Y A D N W F K T Y D P S I N C T V E E M T E A V E G
SEQ. ID. NO. 25	Q I Y R A M N S S S F E G V S G H V V F D A S G S R M A W T
SEQ. ID. NO. 24	H I T T E I V M L N P A N T R S I S N M T S Q E F V E K L T
SEQ. ID. NO. 25	L I E Q L Q G G S Y K K I G Y Y D S T K D D L S W S K T D K
SEQ. ID. NO. 24	K R L K R H P E E T G G F Q E A P L A Y D A I W A L A L A L
SEQ. ID. NO. 25	W I G G S P P A D Q I L V I K T F R F L S Q K L F I S V S V
SEQ. ID. NO. 24	N K T S G G G G R S G V R L E D F N Y N N Q T I T D Q I Y R
SEQ. ID. NO. 25	L S S L G I V L A V V C L S F N I Y N S H V R Y I Q N S Q P
SEQ. ID. NO. 24	A M N S S S F E G V S G H V V F D A S G S R M A W T L I E Q
SEQ. ID. NO. 25	N L N N L T A V G C S L A L A A V F P L G L D G Y H I G R S
SEQ. ID. NO. 24	L Q G G S Y K K I G Y Y D S T K D D L S W S K T D K W I G G
SEQ. ID. NO. 25	Q F P F V C Q A R L W L L G L G F S L G Y G S M F T K I W W
SEQ. ID. NO. 24	S P P A D Q I L V I K T F R F L S Q K L F I S V S V L S S L
SEQ. ID. NO. 25	V H T V F T K K E E K K E W R K T L E P W K L Y A T V G L L
SEQ. ID. NO. 24	G I V L A V V C L S F N I Y N S H V R Y I Q N S Q P N L N N
SEQ. ID. NO. 25	V G M D V L T L A I W Q I V D P L H R T I E T F A K E E P K
SEQ. ID. NO. 24	L T A V G C S L A L A A V F P L G L D G Y H I G R S Q F P F
SEQ. ID. NO. 25	E D I D V S I L P Q L E H C S S K K M N T W L G I F Y G Y K
SEQ. ID. NO. 24	V C Q A R L W L L G L G F S L G Y G S M F T K I W W V H T V
SEQ. ID. NO. 25	G L L L L L G I F L A Y E T K S V S T E K I N D H R A V G M
SEQ. ID. NO. 24	F T K K E E K K E W R K T L E P W K L Y A T V G L L V G M D
SEQ. ID. NO. 25	A I Y N V A V L C L I T A P V T M I L S S Q Q D A A F A F A
SEQ. ID. NO. 24	V L T L A I W Q I V D P L H R T I E T F A K E E P K E D I D
SEQ. ID. NO. 25	S L A I V F S S Y I T L V V L F V P K M R R L I T R G E W Q

FIGURE 7c

SEQ. ID. NO. 24	V S I L P Q L E H C S S K K M N T W L G I F Y G Y K G L L L
SEQ. ID. NO. 25	S E T Q D T M K T G S S T N N N E E E K S R L L E K E N R E

SEQ. ID. NO. 24	L L G I F L A Y E T K S V S T E K I N D H R A V G M A I Y N
SEQ. ID. NO. 25	L E K I I A E K E E R V S E L R H Q L Q S R Q Q L R S R R H

SEQ. ID. NO. 24	V A V L C L I T A P V T M I L S S Q Q D A A F A F A S L A I
SEQ. ID. NO. 25	P P T P P D P S G G L P R G P S E P P D R L S C D G S R V H

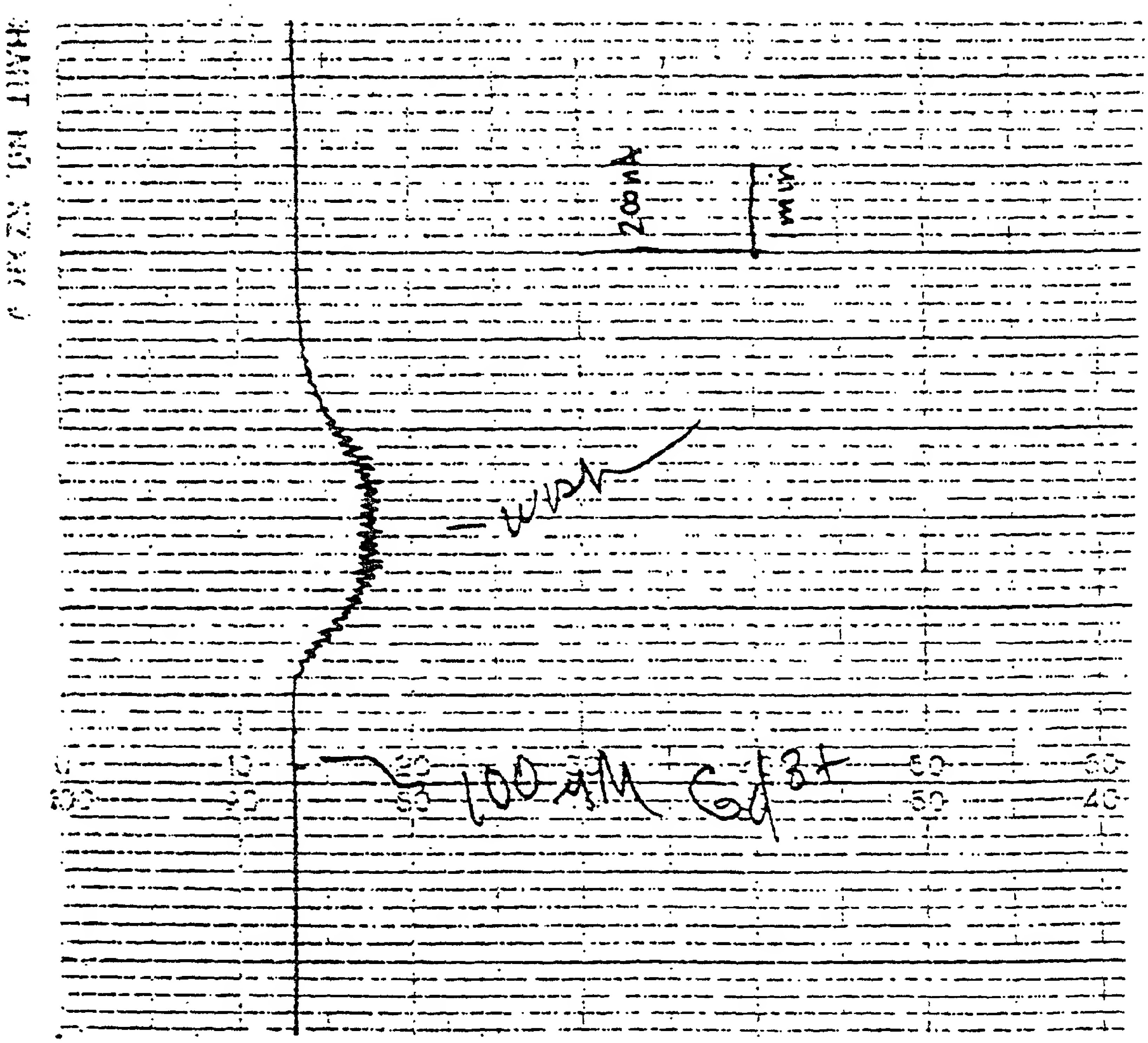
SEQ. ID. NO. 24	V F S S Y I T L V V L F V P K M R R L I T R G E W Q S E T Q
SEQ. ID. NO. 25	L L Y K

SEQ. ID. NO. 24	D T M K T G S S T N N N E E E K S R L L E K E N R E L E K I
SEQ. ID. NO. 25	

SEQ. ID. NO. 24	I A E K E E R V S E L R H Q L Q S R Q Q L R S R R H P P T P
SEQ. ID. NO. 25	

SEQ. ID. NO. 24	P D P S G G L P R G P S E P P D R L S C D G S R V H L L Y K
SEQ. ID. NO. 25	

FIGURE 8



ClustalW Formatted Alignments

SEQ. ID. NO. 38 A T G G T A T G C G A G G G A A A G C G A T C A G
SEQ. ID. NO. 34 A T G G G A T C G C T G C T T G C G C T C C C G G
SEQ. ID. NO. 30 A T G G C A T T T T A T A G C T G C T G C T G G G
SEQ. ID. NO. 26 A T G G G A T C G C T G C T T G C G C T C C T G G

SEQ. ID. NO. 38 C C T C T T G C C C T T G T T T C T T C C T C T T
SEQ. ID. NO. 34 C A C T G C T G C T G C T G T G G G G T G C T G T
SEQ. ID. NO. 30 T C C T C T T G G C A C T C A C C T G G C A C A C
SEQ. ID. NO. 26 C A C T G C T G C C G C T G T G G G G T G C T G T

SEQ. ID. NO. 38 G A C C G C C A A G T T C T A C T G G A T C C T C
SEQ. ID. NO. 34 G G C T G A G G G C C C A G C C A A G A A G G T G
SEQ. ID. NO. 30 C T C T G C C T A C G G G C C A G A C C A G C G A
SEQ. ID. NO. 26 G G C T G A G G G C C C A G C C A A G A A G G T G

SEQ. ID. NO. 38 A C A A T G A T G C A A A G A A C T C A C A G C C
SEQ. ID. NO. 34 C T G A C C C T G G A G G G A G A C T T G G T G C
SEQ. ID. NO. 30 G C C C A A A A G A A G G G G G A C A T T A T C C
SEQ. ID. NO. 26 C T G A C C C T G G A G G G A G A C T T G G T G C

SEQ. ID. NO. 38 A G G A G T A T G C C C A T T C C A T A C G G G T
SEQ. ID. NO. 34 T G G G T G G G C T G T T C C C A G T G C A C C A
SEQ. ID. NO. 30 T T G G G G G G C T C T T T C C T A T T C A T T T
SEQ. ID. NO. 26 T G G G T G G G C T G T T C C C A G T G C A C C A

SEQ. ID. NO. 38 G G A T G G G A C A T T A T T T T G G G G G G T
SEQ. ID. NO. 34 G A A G G G C G G C C C A G C A G A G G A C T G T
SEQ. ID. NO. 30 T G G A G T A G C A G C T A A A G A T C A A G A T
SEQ. ID. NO. 26 G A A G G G C G G C C C A G C A G A G G A C T G T

SEQ. ID. NO. 38 C T C T T C C C T G T C C A C G C A A A G G G A G
SEQ. ID. NO. 34 G G T C C T G T C A A T G A G C A C C G T G G C A
SEQ. ID. NO. 30 C T C A A A T C A A G G C C G G A G T C T G T G G
SEQ. ID. NO. 26 G G T C C T G T C A A T G A G C A C C G T G G C A

SEQ. ID. NO. 38 A G A G A G G G G T G C C T T G T G G G G A G C T
SEQ. ID. NO. 34 T C C A G C G C C T G G A G G C C A T G C T T T T
SEQ. ID. NO. 30 A A T G T A T C A G G T A T A A T T T C C G T G G
SEQ. ID. NO. 26 T C C A G C G C C T G G A G G C C A T G C T T T T

Figure 9a

SEQ. ID. NO. 38	G A A G A A G G A A A A G G G G A T T C A C A G A
SEQ. ID. NO. 34	T G C A C T G G A C C G C A T C A A C C G T G A C
SEQ. ID. NO. 30	G T T T C G C T G G T T A C A G G C T A T G A T A
SEQ. ID. NO. 26	T G C A C T G G A C C G C A T C A A C C G T G A C

SEQ. ID. NO. 38	C T G G A G G C C A T G C T T T A T G C A A T T G
SEQ. ID. NO. 34	C C G C A C C T G C T G C C T G G C G T G C G C C
SEQ. ID. NO. 30	T T T G C C A T A G A G G A G A T A A A C A G C A
SEQ. ID. NO. 26	C C G C A C C T G C T G C C T G G C G T G C G C C

SEQ. ID. NO. 38	A C C A G A T T A A C A A G G A C C C T G A T C T
SEQ. ID. NO. 34	T G G G T G C A C A C A T C C T C G A C A G T T G
SEQ. ID. NO. 30	G C C C A G C C C T T C T T C C C A A C T T G A C
SEQ. ID. NO. 26	T G G G T G C A C A C A T C C T C G A C A G T T G

SEQ. ID. NO. 38	C C T T T C C A A C A T C A C T C T G G G T G T C
SEQ. ID. NO. 34	C T C C A A G G A C A C A C A T G C G C T G G A G
SEQ. ID. NO. 30	G C T G G G A T A C A G G A T A T T T G A C A C T
SEQ. ID. NO. 26	C T C C A A G G A C A C A C A T G C G C T G G A G

SEQ. ID. NO. 38	C G C A T C C T C G A C A C G T G C T C T A G G G
SEQ. ID. NO. 34	C A G G C A C T G G A C T T T G T G C G T G C C T
SEQ. ID. NO. 30	T G C A A C A C C G T T T C T A A G G C C T T G G
SEQ. ID. NO. 26	C A G G C A C T G G A C T T T G T G C G T G C C T

SEQ. ID. NO. 38	A C A C C T A T G C T T T G G A G C A G T C T C T
SEQ. ID. NO. 34	C A C T C A G C C G T G G T G C T G A T G G C T C
SEQ. ID. NO. 30	A A G C C A C C C T G A G T T T T G T T G C T C A
SEQ. ID. NO. 26	C A C T C A G C C G T G G T G C T G A T G G A T C

SEQ. ID. NO. 38	A A C A T T C G T G C A G G C A T T A A T A G A G
SEQ. ID. NO. 34	A C G C C A C A T C T G C C C C G A C G G C T C T
SEQ. ID. NO. 30	A A A C A A A A T T G A T T C T T T G A A C C T T
SEQ. ID. NO. 26	A C G C C A C A T C T G C C C C G A C G G C T C T

SEQ. ID. NO. 38	A A A G A T G C T T C G G A T G T G A A G T G T G
SEQ. ID. NO. 34	T A T G C G A C C C A T G G T G A T G C T C C C A
SEQ. ID. NO. 30	G A T G A G T T C T G C A A C T G C T C A G A G C
SEQ. ID. NO. 26	T A T G C G A C C C A T G G T G A T G C T C C C A

Figure 9b

SEQ. ID. NO. 38	C T A A T G G A G A T C C A C C C A T T T T C A C
SEQ. ID. NO. 34	C T G C C A T C A C T G G T G T T A T T G G C G G
SEQ. ID. NO. 30	A C A T T C C C T C T A C G A T T G C T G T G G T
SEQ. ID. NO. 26	C T G C C A T C A C T G G T G T T A T T G G C G G
SEQ. ID. NO. 38	C A A G C C C G A C A A G A T T T C T G G C G T C
SEQ. ID. NO. 34	T T C C T A C A G T G A T G T C T C C A T C C A G
SEQ. ID. NO. 30	G G G A G C A A C T G G C T C A G G C G T C T C C
SEQ. ID. NO. 26	T T C C T A C A G T G A T G T C T C C A T C C A G
SEQ. ID. NO. 38	A T A G G T G C T G C A G C A A G C T C C G T G T
SEQ. ID. NO. 34	G T G G C C A A C C T C T T G A G G C T A T T T C
SEQ. ID. NO. 30	A C G G C A G T G G C A A A T C T G C T G G G G C
SEQ. ID. NO. 26	G T G G C C A A C C T C T T G A G G C T A T T T C
SEQ. ID. NO. 38	C C A T C A T G G T T G C T A A C A T T T T A A G
SEQ. ID. NO. 34	A G A T C C C A C A G A T T A G C T A C G C C T C
SEQ. ID. NO. 30	T C T T C T A C A T T C C C C A G G T C A G T T A
SEQ. ID. NO. 26	A G A T C C C A C A G A T T A G C T A C G C C T C
SEQ. ID. NO. 38	A C T T T T T A A G A T A C C T C A A A T C A G C
SEQ. ID. NO. 34	T A C C A G T G C C A A G C T G A G T G A C A A G
SEQ. ID. NO. 30	T G C C T C C T C C A G C A G A C T C C T C A G C
SEQ. ID. NO. 26	T A C C A G T G C C A A G C T G A G T G A C A A G
SEQ. ID. NO. 38	T A T G C A T C C A C A G C C C C A G A G C T A A
SEQ. ID. NO. 34	T C C C G C T A T G A C T A C T T T G C C C G C A
SEQ. ID. NO. 30	A A C A A G A A T C A A T T C A A G T C T T T C C
SEQ. ID. NO. 26	T C C C G C T A T G A C T A C T T T G C C C G C A
SEQ. ID. NO. 38	G T G A T A A C A C C A G G T A T G A C T T T T T
SEQ. ID. NO. 34	C A G T G C C T C C T G A C T T C T T C C A A G C
SEQ. ID. NO. 30	T C C G A A C C A T C C C C A A T G A T G A G C A
SEQ. ID. NO. 26	C A G T G C C T C C T G A C T T C T T C C A A G C
SEQ. ID. NO. 38	C T C T C G A G T G G T T C C G C C T G A C T C C
SEQ. ID. NO. 34	C A A G G C C A T G G C T G A G A T T C T C C G C
SEQ. ID. NO. 30	C C A G G C C A C T G C C A T G G C A G A C A T C
SEQ. ID. NO. 26	C A A G G C C A T G G C T G A G A T T C T C C G C

Figure 9c

SEQ. ID. NO. 38 T A C C A A G C C C A A G C C A T G G T G G A C A
SEQ. ID. NO. 34 T T C T T C A A C T G G A C C T A T G T G T C C A
SEQ. ID. NO. 30 A T C G A G T A T T T C C G C T G G A A C T G G G
SEQ. ID. NO. 26 T T C T T C A A C T G G A C C T A T G T G T C C A

SEQ. ID. NO. 38 T C G T G A C A G C A C T G G G A T G G A A T T A
SEQ. ID. NO. 34 C T G T G G C G T C T G A G G G C G A C T A T G G
SEQ. ID. NO. 30 T G G G C A C A A T T G C A G C T G A T G A C G A
SEQ. ID. NO. 26 C T G A G G C C T C T G A G G G C G A C T A T G G

SEQ. ID. NO. 38 T G T T T C G A C A C T G G C T T C T G A G G G G
SEQ. ID. NO. 34 C G A G A C A G G C A T T G A G G C C T T T G A G
SEQ. ID. NO. 30 C T A T G G G C G G C C G G G G A T T G A G A A A
SEQ. ID. NO. 26 C G A G A C A G G C A T T G A G G C C T T T G A G

SEQ. ID. NO. 38 A A C T A T G G T G A G A G C G G T G T G G A G G
SEQ. ID. NO. 34 C T A G A G G C T C G T G C C C G C A A C A T C T
SEQ. ID. NO. 30 T T C C G A G A G G A A G C T G A G G A A A G G G
SEQ. ID. NO. 26 C T A G A G G C T C G T G C C C G C A A C A T C T

SEQ. ID. NO. 38 C C T T C A C C C A G A T C T C G A G G G A G A T
SEQ. ID. NO. 34 G T G T G G C C A C C T C G G A G A A A G T G G G
SEQ. ID. NO. 30 A T A T C T G C A T C G A C T T C A G T G A A C T
SEQ. ID. NO. 26 G T G T G G C C A C C T C G G A G A A A G T G G G

SEQ. ID. NO. 38 T G G T G G T G T T T G C A T T G C T C A G T C A
SEQ. ID. NO. 34 C C G T G C C A T G A G C C G C G C G G C C T T T
SEQ. ID. NO. 30 C A T C T C C C A G T A C T C T G A T G A G G A A
SEQ. ID. NO. 26 C C G T G C C A T G A G C C G C G C G G C C T T T

SEQ. ID. NO. 38 C A G A A A A T C C C A C G T G A A C C A A G A C
SEQ. ID. NO. 34 G A G G G T G T G G T G C G A G C C C T G C T G C
SEQ. ID. NO. 30 G A G A T C C A G C A T G T G G T A G A G G T G A
SEQ. ID. NO. 26 G A G G G T G T G G T G C G A G C C C T G C T G C

SEQ. ID. NO. 38 C T G G A G A A T T T G A A A A A A T T A T C A A
SEQ. ID. NO. 34 A G A A G C C C A G T G C C C G C G T G G C T G T
SEQ. ID. NO. 30 T T C A A A A T T C C A C G G C C A A A G T C A T
SEQ. ID. NO. 26 A G A A G C C C A G T G C C C G C G T G G C T G T

Figure 9d

SEQ. ID. NO. 38	A C G C C T G C T A G A A A C A C C T A A T G C T
SEQ. ID. NO. 34	C C T G T T C A C C C G T T C T G A G G A T G C C
SEQ. ID. NO. 30	C G T G G T T T T C T C C A G T G G C C C A G A T
SEQ. ID. NO. 26	C C T G T T C A C C C G T T C T G A G G A T G C C

SEQ. ID. NO. 38	C G A G C A G T G A T T A T G T T T G C C A A T G
SEQ. ID. NO. 34	C G G G A G C T G C T T G C T G C C A G C C A G C
SEQ. ID. NO. 30	C T T G A G C C C C T C A T C A A G G A G A T T G
SEQ. ID. NO. 26	C G G G A G C T G C T T G C T G C C A G C C A G C

SEQ. ID. NO. 38	A G G A T G A C A T C A G G A G G A T A T T G G A
SEQ. ID. NO. 34	G C C T C A A T G C C A G C T T C A C C T G G G T
SEQ. ID. NO. 30	T C C G G C G C A A T A T C A C G G G C A A G A T
SEQ. ID. NO. 26	G C C T C A A T G C C A G C T T C A C C T G G G T

SEQ. ID. NO. 38	A G C A G C A A A A A A A C T A A A C C A A A G T
SEQ. ID. NO. 34	G G C C A G T G A T G G T T G G G G G G C C C T G
SEQ. ID. NO. 30	C T G G C T G G C C A G C G A G G C C T G G G C C
SEQ. ID. NO. 26	G G C C A G T G A T G G T T G G G G G G C C C T G

SEQ. ID. NO. 38	G G G C A T T T T C T C T G G A T T G G C T C A G
SEQ. ID. NO. 34	G A G A G T G T G G T G G C A G G C A G T G A G G
SEQ. ID. NO. 30	A G C T C C T C C C T G A T C G C C A T G C C T C
SEQ. ID. NO. 26	G A G A G T G T G G T G G C A G G C A G T G A G G

SEQ. ID. NO. 38	A T A G T T G G G G A T C C A A A A T A G C A C C
SEQ. ID. NO. 34	G G G C T G C T G A G G G T G C T A T C A C C A T
SEQ. ID. NO. 30	A G T A C T T C C A C G T G G T T G G C G G C A C
SEQ. ID. NO. 26	G G G C T G C T G A G G G T G C T A T C A C C A T

SEQ. ID. NO. 38	T G T C T A T C A G C A A G A G G A G A T T G C A
SEQ. ID. NO. 34	C G A G C T G G C C T C C T A C C C C A T C A G T
SEQ. ID. NO. 30	C A T T G G A T T C G C T C T G A A G G C T G G G
SEQ. ID. NO. 26	C G A G C T G G C C T C C T A C C C C A T C A G T

SEQ. ID. NO. 38	G A A G G G G C T G T G A C A A T T T T G C C C A
SEQ. ID. NO. 34	G A C T T T G C C T C C T A C T T C C A G A G C C
SEQ. ID. NO. 30	C A G A T C C C A G G C T T C C G G G A A T T C C
SEQ. ID. NO. 26	G A C T T T G C C T C C T A C T T C C A G A G C C

Figure 9e

SEQ. ID. NO. 38 A A C G A G C A T C A A T T G A T G G A T T T G A
SEQ. ID. NO. 34 T G G A C C C T T G G A A C A A C A G C C G G A A
SEQ. ID. NO. 30 T G A A G A A G G T C C A T C C C A G G A A G T C
SEQ. ID. NO. 26 T G G A C C C T T G G A A C A A C A G C C G G A A

SEQ. ID. NO. 38 T C G A T A C T T T A G A A G C C G A A C T C T T
SEQ. ID. NO. 34 C C C C T G G T T C C G T G A A T T C T G G G A G
SEQ. ID. NO. 30 T G T C C A C A A T G G T T T T G C C A A G G A G
SEQ. ID. NO. 26 C C C C T G G T T C C G T G A A T T C T G G G A G

SEQ. ID. NO. 38 G C C A A T A A T C G A A G A A A T G T G T G G T
SEQ. ID. NO. 34 C A G A G G T T C C G C T G C A G C T T C C G G C
SEQ. ID. NO. 30 T T T T G G G A A G A A A C A T T T A A C T G C C
SEQ. ID. NO. 26 C A G A G G T T C C G C T G C A G C T T C C G G C

SEQ. ID. NO. 38 T T G C A G A A T T C T G G G A G G A G A A T T T
SEQ. ID. NO. 34 A G C G A G A C T G C G C A G C C C A C T C T C T
SEQ. ID. NO. 30 A C C T C C A A G A A G G T G C A A A A G G A C C
SEQ. ID. NO. 26 A G C G A G A C T G C G C A G C C C A C T C T C T

SEQ. ID. NO. 38 T G G C T G C A A G T T A G G A T C A C A T G G G
SEQ. ID. NO. 34 C C G G G C T G T G C C C T T T G A G C A G G A G
SEQ. ID. NO. 30 T T T A C C T G T G G A C A C C T T T C T G A G A
SEQ. ID. NO. 26 C C G G G C T G T G C C C T T T G A A C A G G A G

SEQ. ID. NO. 38 A A A A G G A A C A G T C A T A T A A A G A A A T
SEQ. ID. NO. 34 T C C A A G A T C A T G T T T G T G G T C A A T G
SEQ. ID. NO. 30 G G T C A C G A A G A A A G T G G C G A C A G G T
SEQ. ID. NO. 26 T C C A A G A T C A T G T T T G T G G T C A A T G

SEQ. ID. NO. 38 G C A C A G G G C T G G A G C G A A T T G C T C G
SEQ. ID. NO. 34 C A G T G T A C G C C A T G G C C C A T G C G C T
SEQ. ID. NO. 30 T T A G C A A C A G C T C G A C A G C C T T C C G
SEQ. ID. NO. 26 C A G T G T A C G C C A T G G C C C A T G C G C T

SEQ. ID. NO. 38 G G A T T C A T C T T A T G A A C A G G A A G G A
SEQ. ID. NO. 34 C C A C A A C A T G C A C C G T G C C C T C T G C
SEQ. ID. NO. 30 A C C C C T C T G T A C A G G G G A T G A G A A C
SEQ. ID. NO. 26 C C A C A A C A T G C A C C G T G C C C T C T G C

Figure 9f

SEQ. ID. NO. 38 A A G G T C C A A T T T G T A A T T G A T G C T G
SEQ. ID. NO. 34 C C C A A C A C C A C C C G G C T C T G T G A C G
SEQ. ID. NO. 30 A T C A G C A G T G T C G A G A C C C C T T A C A
SEQ. ID. NO. 26 C C C A A C A C C A C C C G G C T C T G T G A C G

SEQ. ID. NO. 38 T A T A T T C C A T G G C T T A C G C C C T G C A
SEQ. ID. NO. 34 C G A T G C G G C C A G T T A A C G G G C G C C G
SEQ. ID. NO. 30 T A G A T T A C A C G C A T T T A C G G A T A T C
SEQ. ID. NO. 26 C G A T G C G G C C A G T T A A C G G G C G C C G

SEQ. ID. NO. 38 C A A T A T G C A C A A A G A T C T C T G C C C T
SEQ. ID. NO. 34 C C T C T A C A A G G A C T T T G T G C T C A A C
SEQ. ID. NO. 30 C T A C A A T G T G T A C T T A G C A G T C T A C
SEQ. ID. NO. 26 C C T C T A C A A G G A C T T T G T G C T C A A C

SEQ. ID. NO. 38 G G A T A C A T T G G C C T T T G T C C A C G A A
SEQ. ID. NO. 34 G T C A A G T T T G A T G C C C C C T T T C G C C
SEQ. ID. NO. 30 T C C A T T G C C C A C G C C T T G C A A G A T A
SEQ. ID. NO. 26 G T C A A G T T T G A T G C C C C C T T T C G C C

SEQ. ID. NO. 38 T G A G T A C C A T T G A T G G G A A A G A G C T
SEQ. ID. NO. 34 C A G C T G A C A C C C A C A A T G A G G T C C G
SEQ. ID. NO. 30 T A T A T A C C T G C T T A C C T G G G A G A G G
SEQ. ID. NO. 26 C A G C T G A C A C C C A C A A T G A G G T C C G

SEQ. ID. NO. 38 A C T T G G T T A T A T T C G G G C T G T A A A T
SEQ. ID. NO. 34 C T T T G A C C G C T T T G G T G A T G G T A T T
SEQ. ID. NO. 30 G C T C T T C A C C A A T G G C T C C T G T G C A
SEQ. ID. NO. 26 C T T T G A C C G C T T T G G T G A T G G T A T T

SEQ. ID. NO. 38 T T T A A T G G C A G T G C T G G C A C T C C T G
SEQ. ID. NO. 34 G G C C G C T A C A A C A T C T T C A C C T A T C
SEQ. ID. NO. 30 G A C A T C A A G A A A G T T G A G G C G T G G C
SEQ. ID. NO. 26 G G C C G C T A C A A C A T C T T C A C C T A T C

SEQ. ID. NO. 38 T C A C T T T T A A T G A A A A C G G A G A T G C
SEQ. ID. NO. 34 T G C G T G C A G G C A G T G G G C G C T A T C G
SEQ. ID. NO. 30 A G G T C C T G A A G C A C C T A C G G C A T C T
SEQ. ID. NO. 26 T G C G T G C A G G C A G T G G G C G C T A T C G

Figure 9g

SEQ. ID. NO. 38	T C C T G G A C G T T A T G A T A T C T T C C A G
SEQ. ID. NO. 34	C T A C C A G A A G G T G G G C T A C T G G G C A
SEQ. ID. NO. 30	A A A C T T T A C A A A C A A T A T G G G G G A G
SEQ. ID. NO. 26	C T A C C A G A A G G T G G G C T A C T G G G C A
SEQ. ID. NO. 38	T A T C A A A T A A C C A A C A A A A G C A C A G
SEQ. ID. NO. 34	G A A G G C T T G A C T C T G G A C A C C A G C C
SEQ. ID. NO. 30	C A G G T G A C C T T T G A T G A G T G T G G T G
SEQ. ID. NO. 26	G A A G G C T T G A C T C T G G A C A C C A G C C
SEQ. ID. NO. 38	A G T A C A A A G T C A T C G G C C A C T G G A C
SEQ. ID. NO. 34	T C A T C C C A T G G G C C T C A C C C T C A G C
SEQ. ID. NO. 30	A C C T G G T G G G G A A C T A T T C C A T C A T
SEQ. ID. NO. 26	T C A T C C C A T G G G C C T C A C C G T C A G C
SEQ. ID. NO. 38	C A A T C A G C T T C A T C T A A A A G T G G A A
SEQ. ID. NO. 34	C G G C C C C C T G C C C G C C T C T C G C T G C
SEQ. ID. NO. 30	C A A C T G G C A C C T C T C C C C A G A G G A T
SEQ. ID. NO. 26	C G G C C C C C T G G C C G C C T C T C G C T G C
SEQ. ID. NO. 38	G A C A T G C A G T G G G C T C A T A G A G A A C
SEQ. ID. NO. 34	A G T G A G C C C T G C C T C C A G A A T G A G G
SEQ. ID. NO. 30	G G C T C C A T C G T G T T T A A G G A A G T C G
SEQ. ID. NO. 26	A G T G A G C C C T G C C T C C A G A A T G A G G
SEQ. ID. NO. 38	A T A C T C A C C C G G C G T C T G T C T G C A G
SEQ. ID. NO. 34	T G A A G A G T G T G C A G C C G G G C G A A G T
SEQ. ID. NO. 30	G G T A T T A C A A C G T C T A T G C C A A G A A
SEQ. ID. NO. 26	T G A A G A G T G T G C A G C C G G G C G A A G T
SEQ. ID. NO. 38	C C T G C C G T G T A A G C C A G G G G A G A G G
SEQ. ID. NO. 34	C T G C T G C T G G C T C T G C A T T C C G T G C
SEQ. ID. NO. 30	G G G A G A A A G A C T C T T C A T C A A C G A G
SEQ. ID. NO. 26	C T G C T G C T G G C T C T G C A T T C C G T G C
SEQ. ID. NO. 38	A A G A A A A C G G T G A A A G G G G T C C C T T
SEQ. ID. NO. 34	C A G C C C T A T G A G T A C C G A T T G G A C G
SEQ. ID. NO. 30	G A G A A A A T C C T G T G G A G T G G G T T C T
SEQ. ID. NO. 26	C A G C C C T A T G A G T A C C G A T T G G A C G

Figure 9h

SEQ. ID. NO. 38	G C T G C T G G C A C T G T G A A C G C T G T G A
SEQ. ID. NO. 34	A A T T C A C T T G C G C T G A T T G T G G C C T
SEQ. ID. NO. 30	C C A G G G A G G T G C C C T T C T C C A A C T G
SEQ. ID. NO. 26	A A T T C A C T T G C G C T G A T T G T G G C C T

SEQ. ID. NO. 38	A G G T T A C A A C T A C C A G G T G G A T G A G
SEQ. ID. NO. 34	G G G C T A C T G G C C C A A T G C C A G C C T G
SEQ. ID. NO. 30	C A G C C G A G A C T G C C T G G C A G G G A C C
SEQ. ID. NO. 26	G G G C T A C T G G C C C A A T G C C A G C C T G

SEQ. ID. NO. 38	C T G T C C T G T G A A C T T T G C C C T C T G G
SEQ. ID. NO. 34	A C T G G C T G C T T C G A A C T G C C C C A G G
SEQ. ID. NO. 30	A G G A A A G G G A T C A T T G A G G G G G A G C
SEQ. ID. NO. 26	A C T G G C T G C T T C G A A C T G C C C C A G G

SEQ. ID. NO. 38	A T C A G A G A C C C A A C A T G A A C C G C A C
SEQ. ID. NO. 34	A G T A C A T C C G C T G G G G C G A T G C C T G
SEQ. ID. NO. 30	C C A C C T G C T G C T T T G A G T G T G T G G A
SEQ. ID. NO. 26	A G T A C A T C C G C T G G G G C G A T G C C T G

SEQ. ID. NO. 38	A G G C T G C C A G C T T A T C C C C A T C A T C
SEQ. ID. NO. 34	G G C T G T G G G A C C T G T C A C C A T C G C C
SEQ. ID. NO. 30	G T G T C C T G A T G G G G A G T A T A G T G A T
SEQ. ID. NO. 26	G G C T G T G G G A C C T G T C A C C A T C G C C

SEQ. ID. NO. 38	A A A T T G G A G T G G C A T T C T C C C T G G G
SEQ. ID. NO. 34	T G C C T C G G T G C C C T G G C C A C C C T C T
SEQ. ID. NO. 30	G A G A C A G A T G C C A G T G C C T G T A A C A
SEQ. ID. NO. 26	T G C C T C G G T G C C C T G G C C A C C C T G T

SEQ. ID. NO. 38	C T G T G G T G C C T G T G T T T G T T G C A A T
SEQ. ID. NO. 34	T T G T G C T G G G T G T C T T T G T G C G G C A
SEQ. ID. NO. 30	A G T G C C C A G A T G A C T T C T G G T C C A A
SEQ. ID. NO. 26	T T G T G C T G G G T G T C T T T G T G C G G C A

SEQ. ID. NO. 38	A T T G G G A A T C A T C G C C A C C A C C T T T
SEQ. ID. NO. 34	C A A T G C C A C A C C A G T G G T C A A G G C C
SEQ. ID. NO. 30	T G A G A A C C A C A C C T C C T G C T T C G A A
SEQ. ID. NO. 26	C A A T G C C A C A C C A G T G G T C A A G G C C

Figure 9i

SEQ. ID. NO. 38 G T G A T C G T G A C C T T T G T C C G C T A T A
SEQ. ID. NO. 34 T C A G G T C G G G A G C T C T G C T A C A T C C
SEQ. ID. NO. 30 C T G C C C C A G G A G T A C A T C C G C T G G G
SEQ. ID. NO. 26 T C A G G T C G G G A G C T C T G C T A C A T C C

SEQ. ID. NO. 38 A T G A C A C A C C T A T C G T G A G G G C T T C
SEQ. ID. NO. 34 T G C T G G G T G G T G T C T T C C T C T G C T A
SEQ. ID. NO. 30 G C G A T G C C T G G G C T G T G G G A C C T G T
SEQ. ID. NO. 26 T G C T G G G T G G T G T C T T C C T C T G C T A

SEQ. ID. NO. 38 A G G A C G C G A A C T T A G T T A C G T G C T C
SEQ. ID. NO. 34 C T G C A T G A C C T T C A T C T T C A T T G C C
SEQ. ID. NO. 30 C A C C A T C G C C T G C C T C G G T G C C C T G
SEQ. ID. NO. 26 C T G C A T G A C C T T C A T C T T C A T T G C C

SEQ. ID. NO. 38 C T A A C G G G G A T T T T T C T C T G T T A T T
SEQ. ID. NO. 34 A A G C C A T C C A C G G C A G T G T G T A C C T
SEQ. ID. NO. 30 G C C A C C C T G T T T G T G C T G G G T G T C T
SEQ. ID. NO. 26 A A G C C A T C C A C G G C A G T G T G T A C C T

SEQ. ID. NO. 38 C A A T C A C G T T T T T A A T G A T T G C A G C
SEQ. ID. NO. 34 T A C G G C G T C T T G G T T T G G G C A C T G C
SEQ. ID. NO. 30 T T G T G C G G C A C A A T G C C A C A C C A G T
SEQ. ID. NO. 26 T A C G G C G T C T T G G T T T G G G C A C T G C

SEQ. ID. NO. 38 A C C A G A T A C A A T C A T A T G C T C C T T C
SEQ. ID. NO. 34 C T T C T C T G T C T G C T A C T C A G C C C T G
SEQ. ID. NO. 30 G G T C A A G G C C T C A G G T C G G G A G C T C
SEQ. ID. NO. 26 C T T C T C T G T C T G C T A C T C A G C C C T G

SEQ. ID. NO. 38 C G A C G G G T C T T C C T A G G A C T T G G C A
SEQ. ID. NO. 34 C T C A C C A A G A C C A A C C G C A T T G C A C
SEQ. ID. NO. 30 T G C T A C A T C C T G C T G G G T G G T G T C T
SEQ. ID. NO. 26 C T C A C C A A G A C C A A C C G C A T T G C A C

SEQ. ID. NO. 38 T G T G T T T C A G C T A T G C A G C C C T T C T
SEQ. ID. NO. 34 G C A T C T T C G G T G G G G C C C G G G A G G G
SEQ. ID. NO. 30 T C C T C T G C T A C T G C A T G A C C T T C A T
SEQ. ID. NO. 26 G C A T C T T C G G T G G G G C C C G G G A G G G

Figure 9j

SEQ. ID. NO. 38 G A C C A A A A C A A A C C G T A T C C A C C G A
SEQ. ID. NO. 34 T G C C C A G C G G C C A C G C T T C A T C A G T
SEQ. ID. NO. 30 C T T C A T T G C C A A G C C A T C C A C G G C A
SEQ. ID. NO. 26 T G C C C A G C G G C C A C G C T T C A T C A G T

SEQ. ID. NO. 38 A T A T T T G A G C A G G G G A A G A A A T C T G
SEQ. ID. NO. 34 C C T G C C T C A C A G G T G G C C A T C T G C C
SEQ. ID. NO. 30 G T G T G T A C C T T A C G G C G T C T T G G T T
SEQ. ID. NO. 26 C C T G C C T C A C A G G T G G C C A T C T G C C

SEQ. ID. NO. 38 T C A C A G C G C C C A A G T T C A T T A G T C C
SEQ. ID. NO. 34 T G G C A C T T A T C T C G G G C C A G C T G C T
SEQ. ID. NO. 30 T G G G C A C T G C C T T C T C T G T C T G C T A
SEQ. ID. NO. 26 T G G C A C T T A T C T C G G G C C A G C T G C T

SEQ. ID. NO. 38 A G C A T C T C A G C T G G T G A T C A C C T T C
SEQ. ID. NO. 34 C A T C G T G G T C G C C T G G C T G G T G G T G
SEQ. ID. NO. 30 C T C A G C C C T G C T C A C C A A G A C C A A C
SEQ. ID. NO. 26 C A T C G T G G T C G C C T G G C T G G T G G T G

SEQ. ID. NO. 38 A G C C T C A T C T C C G T C C A G C T C C T T G
SEQ. ID. NO. 34 G A G G C A C C G G G C A C A G G C A A G G A G A
SEQ. ID. NO. 30 C G C A T T G C A C G C A T C T T C G G T G G G G
SEQ. ID. NO. 26 G A G G C A C C G G G C A C A G G C A A G G A G A

SEQ. ID. NO. 38 G A G T G T T T G T C T G G T T T G T T G T G G A
SEQ. ID. NO. 34 C A G C C C C C G A A C G G C G G G A G G T G G T
SEQ. ID. NO. 30 C C C G G G A G G G T G C C C A G C G G C C A C G
SEQ. ID. NO. 26 C A G C C C C C G A A C G G C G G G A G G T G G T

SEQ. ID. NO. 38 T C C C C C C C A C A T C A T C A T T G A C T A T
SEQ. ID. NO. 34 G A C A C T G C G C T G C A A C C A C C G C G A T
SEQ. ID. NO. 30 C T T C A T C A G T C C T G C C T C A C A G G T G
SEQ. ID. NO. 26 G A C A C T G C G C T G C A A C C A C C G C G A T

SEQ. ID. NO. 38 G G A G A G C A G C G G A C A C T A G A T C C A G
SEQ. ID. NO. 34 G C A A G T A T G T T G G G C T C G C T G G C C T
SEQ. ID. NO. 30 G C C A T C T G C C T G G C A C T T A T C T C G G
SEQ. ID. NO. 26 G C A A G T A T G T T G G G C T C G C T G G C C T

Figure 9k

SEQ. ID. NO. 38	A G A A G G C C A G G G G A G T G C T C A A G T G
SEQ. ID. NO. 34	A C A A T G T G C T C C T C A T C G C G C T C T G
SEQ. ID. NO. 30	G C C A G C T G C T C A T C G T G G T C G C C T G
SEQ. ID. NO. 26	A C A A T G T G C T C C T C A T C G C G C T C T G

SEQ. ID. NO. 38	T G A C A T T T C T G A T C T C T C A C T C A T T
SEQ. ID. NO. 34	C A C G C T T T A T G C C T T C A A G A C T C G C
SEQ. ID. NO. 30	G C T G G T G G T G G A G G C A C C G G G C A C A
SEQ. ID. NO. 26	C A C G C T T T A T G C C T T C A A T A C T C G C

SEQ. ID. NO. 38	T G T T C A C T T G G A T A C A G T A T C C T C T
SEQ. ID. NO. 34	A A G T G C C C C G A A A A C T T C A A C G A G G
SEQ. ID. NO. 30	G G C A A G G A G A C A G C C C C C G A A C G G C
SEQ. ID. NO. 26	A A G T G C C C C G A A A A C T T C A A C G A G G

SEQ. ID. NO. 38	T G A T G G T C A C T T G T A C T G T T T A T G C
SEQ. ID. NO. 34	C C A A G T T C A T T G G C T T C A C C A T G T A
SEQ. ID. NO. 30	G G G A G G T G G T G A C A C T G C G C T G C A A
SEQ. ID. NO. 26	C C A A G T T C A T T G G C T T C A C C A T G T A

SEQ. ID. NO. 38	C A T T A A A A C G A G A G G T G T C C C A G A G
SEQ. ID. NO. 34	C A C C A C C T G C A T C A T C T G G C T G G C A
SEQ. ID. NO. 30	C C A C C G C G A T G C A A G T A T G T T G G G C
SEQ. ID. NO. 26	C A C C A C C T G C A T C A T C T G G C T G G C A

SEQ. ID. NO. 38	A C T T T C A A T G A A G C C A A A C C T A T T G
SEQ. ID. NO. 34	T T C C T G C C C A T C T T C T A T G T C A C C T
SEQ. ID. NO. 30	T C G C T G G C C T A C A A T G T G C T C C T C A
SEQ. ID. NO. 26	T T G T T G C C C A T C T T C T A T G T C A C C T

SEQ. ID. NO. 38	G A T T T A C C A T G T A T A C C A C C T G C A T
SEQ. ID. NO. 34	C C A G T G A C T A C C G G G T A C A G A C C A C
SEQ. ID. NO. 30	T C G C G C T C T G C A C G C T T T A T G C C T T
SEQ. ID. NO. 26	C C A G T G A C T A C C G G G T A C A G A C C A C

SEQ. ID. NO. 38	C A T T T G G T T A G C T T T C A T C C C C A T C
SEQ. ID. NO. 34	C A C C A T G T G C G T G T C A G T C A G C C T C
SEQ. ID. NO. 30	C A A T A C T C G C A A G T G C C C C G A A A A C
SEQ. ID. NO. 26	C A C C A T G T G C G T G T C A G T C A G C C T C

Figure 91

SEQ. ID. NO. 38 T T T T T T G G T A C A G C C C A G T C A G C A G
SEQ. ID. NO. 34 A G C G G C T C C G T G G T G C T T G G C T G C C
SEQ. ID. NO. 30 T T C A A C G A G G C C A A G T T C A T T G G C T
SEQ. ID. NO. 26 A G C G G C T C C G T G G T G C T T G G C T G C C

SEQ. ID. NO. 38 A A A A G A T G T A C A T C C A G A C A A C A A C
SEQ. ID. NO. 34 T C T T T G C G C C C A A G C T G C A C A T C A T
SEQ. ID. NO. 30 T C A C C A T G T A C A C C A C C T G C A T C A T
SEQ. ID. NO. 26 T C T T T G C G C C C A A G C T G C A C A T C A T

SEQ. ID. NO. 38 A C T T A C T G T C T C C A T G A G T T T A A G T
SEQ. ID. NO. 34 C C T C T T C C A G C C G C A G A A G A A C A C C
SEQ. ID. NO. 30 C T G G C T G G C A T T G T T G C C C A T C T T C
SEQ. ID. NO. 26 C C T C T T C C A G C C G C A G A A G A A C G T G

SEQ. ID. NO. 38 G C T T C A G T A T C T C T G G G C A T G C T C T
SEQ. ID. NO. 34 A T C G A G G A G G T G C G T T G C A G C A C C G
SEQ. ID. NO. 30 T A T G T C A C C T C C A G T G A C T A C C G G G
SEQ. ID. NO. 26 G T T A G C C A C C G G G C A C C C A C C A G C C

SEQ. ID. NO. 38 A T A T G C C C A A G G T T T A T A T T A T A A T
SEQ. ID. NO. 34 C A G C T C A C G C T T T C A A G G T G G C T G C
SEQ. ID. NO. 30 T A C A G A C C A C C A C C A T G T G C G T G T C
SEQ. ID. NO. 26 G C T T T G G C A G T G C T G C T G C C A G G G C

SEQ. ID. NO. 38 T T T T C A T C C A G A A C A G A A T A C C A T C
SEQ. ID. NO. 34 C C G G G C C A C G C T G C G C C G C A G C A A C
SEQ. ID. NO. 30 A G T C A G C C T C A G C G G C T C C G T G G T G
SEQ. ID. NO. 26 C A G C T C C A G C C T T G G C C A A G G G T C T

SEQ. ID. NO. 38 G A G G A G G T G C G T T G C A G C A C C G C A G
SEQ. ID. NO. 34 G T C T C C C G C A A G C G G T C C A G C A G C C
SEQ. ID. NO. 30 C T T G G C T G C C T C T T T G C G C C C A A G C
SEQ. ID. NO. 26 G G C T C C C A G T T T G T C C C C A C T G T T T

SEQ. ID. NO. 38 C T C A C G C T T T C A A G G T G G C T G C C C G
SEQ. ID. NO. 34 T T G G A G G C T C C A C G G G A T C C A C C C C
SEQ. ID. NO. 30 T G C A C A T C A T C C T C T T C C A G C C G C A
SEQ. ID. NO. 26 G C A A T G G C C G T G A G G T G G T G G A C T C

Figure 9m

SEQ. ID. NO. 38 G G C C A C G C T G C G C C G C A G C A A C G T C
SEQ. ID. NO. 34 C T C C T C C T C C A T C A G C A G C A A G A G C
SEQ. ID. NO. 30 G A A G A A C G T G G T T A G C C A C C G G G C A
SEQ. ID. NO. 26 G A C A A C G T C A T C G C T T

SEQ. ID. NO. 38 T C C C G C A A G C G G T C C A G C A G C C T T G
SEQ. ID. NO. 34 A A C A G C G A A G A C C C A T T C C C A C A G C
SEQ. ID. NO. 30 C C C A C C A G C C G C T T T G G C A G T G C T G
SEQ. ID. NO. 26

SEQ. ID. NO. 38 G A G G C T C C A C G G G A T C C A C C C C C T C
SEQ. ID. NO. 34 C C G A G A G G C A G A A G C A G C A G C A G C C
SEQ. ID. NO. 30 C T G C C A G G G C C A G C T C C A G C C T T G G
SEQ. ID. NO. 26

SEQ. ID. NO. 38 C T C C T C C A T C A G C A G C A A G A G C A A C
SEQ. ID. NO. 34 G C T G G C C C T A A C C C A G C A A G A G C A G
SEQ. ID. NO. 30 C C A A G G G T C T G G C T C C C A G T T T G T C
SEQ. ID. NO. 26

SEQ. ID. NO. 38 A G C G A A G A C C C A T T C C C A C A G C C C G
SEQ. ID. NO. 34 C A G C A G C A G C C C C T G A C C C T C C C A C
SEQ. ID. NO. 30 C C C A C T G T T T G C A A T G G C C G T G A G G
SEQ. ID. NO. 26

SEQ. ID. NO. 38 A G A G G C A G A A G C A G C A G C A G C C G C T
SEQ. ID. NO. 34 A G C A G C A A C G A T C T C A G C A G C A G C C
SEQ. ID. NO. 30 T G G T G G A C T C G A C A A C G T C A T C G C T
SEQ. ID. NO. 26

SEQ. ID. NO. 38 G G C C C T A A C C C A G C A A G A G C A G C A G
SEQ. ID. NO. 34 C A G A T G C A A G C A G A A G G T C A T C T T T
SEQ. ID. NO. 30 T
SEQ. ID. NO. 26

SEQ. ID. NO. 38 C A G C A G C C C C T G A C C C T C C C A C A G C
SEQ. ID. NO. 34 G G C A G C G G C A C G G T C A C C T T C T C A C
SEQ. ID. NO. 30
SEQ. ID. NO. 26

Figure 9n

SEQ. ID. NO. 38 A G C A A C G A T C T C A G C A G C A G C C C A G
SEQ. ID. NO. 34 T G A G C T T T G A T G A G C C T C A G A A G A A
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 A T G C A A G C A G A A G G T C A T C T T T G G C
SEQ. ID. NO. 34 C G C C A T G G C C C A C G G G A A T T C T A C G
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 A G C G G C A C G G T C A C C T T C T C A C T G A
SEQ. ID. NO. 34 C A C C A G A A C T C C C T G G A G G C C C A G A
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 G C T T T G A T G A G C C T C A G A A G A A C G C
SEQ. ID. NO. 34 A A A G C A G C G A T A C G C T G A C C C G A C A
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 C A T G G C C C A C G G G A A T T C T A C G C A C
SEQ. ID. NO. 34 C C A G C C A T T A C T C C C G C T G C A G T G C
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 C A G A A C T C C C T G G A G G C C C A G A A A A
SEQ. ID. NO. 34 G G G G A A A C G G A C T T A G A T C T G A C C G
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 G C A G C G A T A C G C T G A C C C G A C A C C A
SEQ. ID. NO. 34 T C C A G G A A A C A G G T C T G C A A G G A C C
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 G C C A T T A C T C C C G C T G C A G T G C G G G
SEQ. ID. NO. 34 T G T G G G T G G A G A C C A G C G G C C A G A G
SEQ. ID. NO. 30
SEQ. ID. NO. 26

Figure 9o

SEQ. ID. NO. 38	G A A A C G G A C T T A G A T C T G A C C G T C C
SEQ. ID. NO. 34	G T G G A G G A C C C T G A A G A G T T G T C C C
SEQ. ID. NO. 30	
SEQ. ID. NO. 26	

SEQ. ID. NO. 38	A G G A A A C A G G T C T G C A A G G A C C T G T
SEQ. ID. NO. 34	C A G C A C T T G T A G T G T C C A G T T C A C A
SEQ. ID. NO. 30	
SEQ. ID. NO. 26	

SEQ. ID. NO. 38	G G G T G G A G A C C A G C G G C C A G A G G T G
SEQ. ID. NO. 34	G A G C T T T G T C A T C A G T G G T G G A G G C
SEQ. ID. NO. 30	
SEQ. ID. NO. 26	

SEQ. ID. NO. 38	G A G G A C C C T G A A G A G T T G T C C C C A G
SEQ. ID. NO. 34	A G C A C T G T T A C A G A A A A C G T A G T G A
SEQ. ID. NO. 30	
SEQ. ID. NO. 26	

SEQ. ID. NO. 38	C A C T T G T A G T G T C C A G T T C A C A G A G
SEQ. ID. NO. 34	A T T C A
SEQ. ID. NO. 30	
SEQ. ID. NO. 26	

SEQ. ID. NO. 38	C T T T G T C A T C A G T G G T G G A G G C A G C
SEQ. ID. NO. 34	
SEQ. ID. NO. 30	
SEQ. ID. NO. 26	

SEQ. ID. NO. 38	A C T G T T A C A G A A A A C G T A G T G A A T T
SEQ. ID. NO. 34	
SEQ. ID. NO. 30	
SEQ. ID. NO. 26	

SEQ. ID. NO. 38	C A
SEQ. ID. NO. 34	
SEQ. ID. NO. 30	
SEQ. ID. NO. 26	

Figure 9p

ClustalW Formatted Alignments

SEQ. ID. NO. 39	M V C E G K R S A S C P C F F L L T A K F Y W I L
SEQ. ID. NO. 35	M G S L L A L P A L L L L W G A V A E G P A K K V
SEQ. ID. NO. 31	M A F Y S C C W V L L A L T W H T S A Y G P D Q R
SEQ. ID. NO. 27	M G S L L A L L A L L P L W G A V A E G P A K K V

SEQ. ID. NO. 39	T M M Q R T H S Q E Y A H S I R V D G D I I L G G
SEQ. ID. NO. 35	L T L E G D L V L G G L F P V H Q K G G P A E D C
SEQ. ID. NO. 31	A Q K K G D I I L G G L F P I H F G V A A K D Q D
SEQ. ID. NO. 27	L T L E G D L V L G G L F P V H Q K G G P A E D C

SEQ. ID. NO. 39	L F P V H A K G E R G V P C G E L K K E K G I H R
SEQ. ID. NO. 35	G P V N E H R G I Q R L E A M L F A L D R I N R D
SEQ. ID. NO. 31	L K S R P E S V E C I R Y N F R G F R W L Q A M I
SEQ. ID. NO. 27	G P V N E H R G I Q R L E A M L F A L D R I N R D

SEQ. ID. NO. 39	L E A M L Y A I D Q I N K D P D L L S N I T L G V
SEQ. ID. NO. 35	P H L L P G V R L G A H I L D S C S K D T H A L E
SEQ. ID. NO. 31	F A I E E I N S S P A L L P N L T L G Y R I F D T
SEQ. ID. NO. 27	P H L L P G V R L G A H I L D S C S K D T H A L E

SEQ. ID. NO. 39	R I L D T C S R D T Y A L E Q S L T F V Q A L I E
SEQ. ID. NO. 35	Q A L D F V R A S L S R G A D G S R H I C P D G S
SEQ. ID. NO. 31	C N T V S K A L E A T L S F V A Q N K I D S L N L
SEQ. ID. NO. 27	Q A L D F V R A S L S R G A D G S R H I C P D G S

SEQ. ID. NO. 39	K D A S D V K C A N G D P P I F T K P D K I S G V
SEQ. ID. NO. 35	Y A T H G D A P T A I T G V I G G S Y S D V S I Q
SEQ. ID. NO. 31	D E F C N C S E H I P S T I A V V G A T G S G V S
SEQ. ID. NO. 27	Y A T H G D A P T A I T G V I G G S Y S D V S I Q

SEQ. ID. NO. 39	I G A A A S S V S I M V A N I L R L F K I P Q I S
SEQ. ID. NO. 35	V A N L L R L F Q I P Q I S Y A S T S A K L S D K
SEQ. ID. NO. 31	T A V A N L L G L F Y I P Q V S Y A S S S R L L S
SEQ. ID. NO. 27	V A N L L R L F Q I P Q I S Y A S T S A K L S D K

SEQ. ID. NO. 39	Y A S T A P E L S D N T R Y D F F S R V V P P D S
SEQ. ID. NO. 35	S R Y D Y F A R T V P P D F F Q A K A M A E I L R
SEQ. ID. NO. 31	N K N Q F K S F L R T I P N D E H Q A T A M A D I
SEQ. ID. NO. 27	S R Y D Y F A R T V P P D F F Q A K A M A E I L R

Figure 10a

SEQ. ID. NO. 39	Y Q A Q A M V D I V T A L G W N Y V S T L A S E G
SEQ. ID. NO. 35	F F N W T Y V S T V A S E G D Y G E T G I E A F E
SEQ. ID. NO. 31	I E Y F R W N W V G T I A A D D D Y G R P G I E K
SEQ. ID. NO. 27	F F N W T Y V S T E A S E G D Y G E T G I E A F E
SEQ. ID. NO. 39	N Y G E S G V E A F T Q I S R E I G G V C I A Q S
SEQ. ID. NO. 35	L E A R A R N I C V A T S E K V G R A M S R A A F
SEQ. ID. NO. 31	F R E E A E E R D I C I D F S E L I S Q Y S D E E
SEQ. ID. NO. 27	L E A R A R N I C V A T S E K V G R A M S R A A F
SEQ. ID. NO. 39	Q K I P R E P R P G E F E K I I K R L L E T P N A
SEQ. ID. NO. 35	E G V V R A L L Q K P S A R V A V L F T R S E D A
SEQ. ID. NO. 31	E I Q H V V E V I Q N S T A K V I V V F S S G P D
SEQ. ID. NO. 27	E G V V R A L L Q K P S A R V A V L F T R S E D A
SEQ. ID. NO. 39	R A V I M F A N E D D I R R I L E A A K K L N Q S
SEQ. ID. NO. 35	R E L L A A S Q R L N A S F T W V A S D G W G A L
SEQ. ID. NO. 31	L E P L I K E I V R R N I T G K I W L A S E A W A
SEQ. ID. NO. 27	R E L L A A S Q R L N A S F T W V A S D G W G A L
SEQ. ID. NO. 39	G H F L W I G S D S W G S K I A P V Y Q Q E E I A
SEQ. ID. NO. 35	E S V V A G S E G A A E G A I T I E L A S Y P I S
SEQ. ID. NO. 31	S S S L I A M P Q Y F H V V G G T I G F A L K A G
SEQ. ID. NO. 27	E S V V A G S E G A A E G A I T I E L A S Y P I S
SEQ. ID. NO. 39	E G A V T I L P K R A S I D G F D R Y F R S R T L
SEQ. ID. NO. 35	D F A S Y F Q S L D P W N N S R N P W F R E F W E
SEQ. ID. NO. 31	Q I P G F R E F L K K V H P R K S V H N G F A K E
SEQ. ID. NO. 27	D F A S Y F Q S L D P W N N S R N P W F R E F W E
SEQ. ID. NO. 39	A N N R R N V W F A E F W E E N F G C K L G S H G
SEQ. ID. NO. 35	Q R F R C S F R Q R D C A A H S L R A V P F E Q E
SEQ. ID. NO. 31	F W E E T F N C H L Q E G A K G P L P V D T F L R
SEQ. ID. NO. 27	Q R F R C S F R Q R D C A A H S L R A V P F E Q E
SEQ. ID. NO. 39	K R N S H I K K C T G L E R I A R D S S Y E Q E G
SEQ. ID. NO. 35	S K I M F V V N A V Y A M A H A L H N M H R A L C
SEQ. ID. NO. 31	G H E E S G D R F S N S S T A F R P L C T G D E N
SEQ. ID. NO. 27	S K I M F V V N A V Y A M A H A L H N M H R A L C

Figure 10b

SEQ. ID. NO. 39	K V Q F V I D A V Y S M A Y A L H N M H K D L C P
SEQ. ID. NO. 35	P N T T R L C D A M R P V N G R R L Y K D F V L N
SEQ. ID. NO. 31	I S S V E T P Y I D Y T H L R I S Y N V Y L A V Y
SEQ. ID. NO. 27	P N T T R L C D A M R P V N G R R L Y K D F V L N
SEQ. ID. NO. 39	G Y I G L C P R M S T I D G K E L L G Y I R A V N
SEQ. ID. NO. 35	V K F D A P F R P A D T H N E V R F D R F G D G I
SEQ. ID. NO. 31	S I A H A L Q D I Y T C L P G R G L F T N G S C A
SEQ. ID. NO. 27	V K F D A P F R P A D T H N E V R F D R F G D G I
SEQ. ID. NO. 39	F N G S A G T P V T F N E N G D A P G R Y D I F Q
SEQ. ID. NO. 35	G R Y N I F T Y L R A G S G R Y R Y Q K V G Y W A
SEQ. ID. NO. 31	D I K K V E A W Q V L K H L R H L N F T N N M G E
SEQ. ID. NO. 27	G R Y N I F T Y L R A G S G R Y R Y Q K V G Y W A
SEQ. ID. NO. 39	Y Q I T N K S T E Y K V I G H W T N Q L H L K V E
SEQ. ID. NO. 35	E G L T L D T S L I P W A S P S A G P L P A S R C
SEQ. ID. NO. 31	Q V T F D E C G D L V G N Y S I I N W H L S P E D
SEQ. ID. NO. 27	E G L T L D T S L I P W A S P S A G P L A A S R C
SEQ. ID. NO. 39	D M Q W A H R E H T H P A S V C S L P C K P G E R
SEQ. ID. NO. 35	S E P C L Q N E V K S V Q P G E V C C W L C I P C
SEQ. ID. NO. 31	G S I V F K E V G Y Y N V Y A K K G E R L F I N E
SEQ. ID. NO. 27	S E P C L Q N E V K S V Q P G E V C C W L C I P C
SEQ. ID. NO. 39	K K T V K G V P C C W H C E R C E G Y N Y Q V D E
SEQ. ID. NO. 35	Q P Y E Y R L D E F T C A D C G L G Y W P N A S L
SEQ. ID. NO. 31	E K I L W S G F S R E V P F S N C S R D C L A G T
SEQ. ID. NO. 27	Q P Y E Y R L D E F T C A D C G L G Y W P N A S L
SEQ. ID. NO. 39	L S C E L C P L D Q R P N M N R T G C Q L I P I I
SEQ. ID. NO. 35	T G C F E L P Q E Y I R W G D A W A V G P V T I A
SEQ. ID. NO. 31	R K G I I E G E P T C C F E C V E C P D G E Y S D
SEQ. ID. NO. 27	T G C F E L P Q E Y I R W G D A W A V G P V T I A
SEQ. ID. NO. 39	K L E W H S P W A V V P V F V A I L G I I A T T F
SEQ. ID. NO. 35	C L G A L A T L F V L G V F V R H N A T P V V K A
SEQ. ID. NO. 31	E T D A S A C N K C P D D F W S N E N H T S C F E
SEQ. ID. NO. 27	C L G A L A T L F V L G V F V R H N A T P V V K A

Figure 10c

SEQ. ID. NO. 39	V I V T F V R Y N D T P I V R A S G R E L S Y V L
SEQ. ID. NO. 35	S G R E L C Y I L L G G V F L C Y C M T F I F I A
SEQ. ID. NO. 31	L P Q E Y I R W G D A W A V G P V T I A C L G A L
SEQ. ID. NO. 27	S G R E L C Y I L L G G V F L C Y C M T F I F I A
SEQ. ID. NO. 39	L T G I F L C Y S I T F L M I A A P D T I I C S F
SEQ. ID. NO. 35	K P S T A V C T L R R L G L G T A F S V C Y S A L
SEQ. ID. NO. 31	A T L F V L G V F V R H N A T P V V K A S G R E L
SEQ. ID. NO. 27	K P S T A V C T L R R L G L G T A F S V C Y S A L
SEQ. ID. NO. 39	R R V F L G L G M C F S Y A A L L T K T N R I H R
SEQ. ID. NO. 35	L T K T N R I A R I F G G A R E G A Q R P R F I S
SEQ. ID. NO. 31	C Y I L L G G V F L C Y C M T F I F I A K P S T A
SEQ. ID. NO. 27	L T K T N R I A R I F G G A R E G A Q R P R F I S
SEQ. ID. NO. 39	I F E Q G K K S V T A P K F I S P A S Q L V I T F
SEQ. ID. NO. 35	P A S Q V A I C L A L I S G Q L L I V V A W L V V
SEQ. ID. NO. 31	V C T L R R L G L G T A F S V C Y S A L L T K T N
SEQ. ID. NO. 27	P A S Q V A I C L A L I S G Q L L I V V A W L V V
SEQ. ID. NO. 39	S L I S V Q L L G V F V W F V V D P P H I I I D Y
SEQ. ID. NO. 35	E A P G T G K E T A P E R R E V V T L R C N H R D
SEQ. ID. NO. 31	R I A R I F G G A R E G A Q R P R F I S P A S Q V
SEQ. ID. NO. 27	E A P G T G K E T A P E R R E V V T L R C N H R D
SEQ. ID. NO. 39	G E Q R T L D P E K A R G V L K C D I S D L S L I
SEQ. ID. NO. 35	A S M L G S L A Y N V L L I A L C T L Y A F K T R
SEQ. ID. NO. 31	A I C L A L I S G Q L L I V V A W L V V E A P G T
SEQ. ID. NO. 27	A S M L G S L A Y N V L L I A L C T L Y A F N T R
SEQ. ID. NO. 39	C S L G Y S I L L M V T C T V Y A I K T R G V P E
SEQ. ID. NO. 35	K C P E N F N E A K F I G F T M Y T T C I I W L A
SEQ. ID. NO. 31	G K E T A P E R R E V V T L R C N H R D A S M L G
SEQ. ID. NO. 27	K C P E N F N E A K F I G F T M Y T T C I I W L A
SEQ. ID. NO. 39	T F N E A K P I G F T M Y T T C I I W L A F I P I
SEQ. ID. NO. 35	F L P I F Y V T S S D Y R V Q T T T M C V S V S L
SEQ. ID. NO. 31	S L A Y N V L L I A L C T L Y A F N T R K C P E N
SEQ. ID. NO. 27	L L P I F Y V T S S D Y R V Q T T T M C V S V S L

Figure 10d

SEQ. ID. NO. 39	F F G T A Q S A E K M Y I Q T T T L T V S M S L S
SEQ. ID. NO. 35	S G S V V L G C L F A P K L H I I L F Q P Q K N T
SEQ. ID. NO. 31	F N E A K F I G F T M Y T T C I I W L A L L P I F
SEQ. ID. NO. 27	S G S V V L G C L F A P K L H I I L F Q P Q K N

SEQ. ID. NO. 39	A S V S L G M L Y M P K V Y I I I F H P E Q N T I
SEQ. ID. NO. 35	I E E V R C S T A A H A F K V A A R A T L R R S N
SEQ. ID. NO. 31	Y V T S S D Y R V Q T T T M C V S V S L S G S V V
SEQ. ID. NO. 27	

SEQ. ID. NO. 39	E E V R C S T A A H A F K V A A R A T L R R S N V
SEQ. ID. NO. 35	V S R K R S S S L G G S T G S T P S S S I S S K S
SEQ. ID. NO. 31	L G C L F A P K L H I I L F Q P Q K N V V S H R A
SEQ. ID. NO. 27	

SEQ. ID. NO. 39	S R K R S S S L G G S T G S T P S S S I S S K S N
SEQ. ID. NO. 35	N S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q
SEQ. ID. NO. 31	P T S R F G S A A A R A S S S L G Q G S G S Q F V
SEQ. ID. NO. 27	

SEQ. ID. NO. 39	S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q Q
SEQ. ID. NO. 35	Q Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F
SEQ. ID. NO. 31	P T V C N G R E V V D S T T S S L
SEQ. ID. NO. 27	

SEQ. ID. NO. 39	Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F G
SEQ. ID. NO. 35	G S G T V T F S L S F D E P Q K N A M A H G N S T
SEQ. ID. NO. 31	
SEQ. ID. NO. 27	

SEQ. ID. NO. 39	S G T V T F S L S F D E P Q K N A M A H G N S T H
SEQ. ID. NO. 35	H Q N S L E A Q K S S D T L T R H Q P L L P L Q C
SEQ. ID. NO. 31	
SEQ. ID. NO. 27	

SEQ. ID. NO. 39	Q N S L E A Q K S S D T L T R H Q P L L P L Q C G
SEQ. ID. NO. 35	G E T D L D L T V Q E T G L Q G P V G G D Q R P E
SEQ. ID. NO. 31	
SEQ. ID. NO. 27	

Figure 10e

SEQ. ID. NO. 39	E T D L D L T V Q E T G L Q G P V G G D Q R P E V
SEQ. ID. NO. 35	V E D P E E L S P A L V V S S S Q S F V I S G G G
SEQ. ID. NO. 31	
SEQ. ID. NO. 27	

SEQ. ID. NO. 39	E D P E E L S P A L V V S S S Q S F V I S G G G S
SEQ. ID. NO. 35	S T V T E N V V N S
SEQ. ID. NO. 31	
SEQ. ID. NO. 27	

SEQ. ID. NO. 39	T V T E N V V N S
SEQ. ID. NO. 35	
SEQ. ID. NO. 31	
SEQ. ID. NO. 27	

Figure 10f

ClustalW Formatted Alignments

SEQ. ID. NO. 40	A T G G T A T G C G A G G G A A A G C G A T C A G
SEQ. ID. NO. 46	A T G G G A T C G C T G C T T G C G C T C C C G G
SEQ. ID. NO. 36	A T G G G A T C G C T G C T T G C G C T C C C G G
SEQ. ID. NO. 32	A T G G C A T T T T A T A G C T G C T G C T G G G
SEQ. ID. NO. 40	C C T C T T G C C C T T G T T T C T T C C T C T T
SEQ. ID. NO. 46	C A C T G C T G C T G C T G T G G G G T G C T G T
SEQ. ID. NO. 36	C A C T G C T G C T G C T G T G G G G T G C T G T
SEQ. ID. NO. 32	T C C T C T T G G C A C T C A C C T G G C A C A C
SEQ. ID. NO. 40	G A C C G C C A A G T T C T A C T G G A T C C T C
SEQ. ID. NO. 46	G G C T G A G G G C C C A G C C A A G A A G G T G
SEQ. ID. NO. 36	G G C T G A G G G C C C A G C C A A G A A G G T G
SEQ. ID. NO. 32	C T C T G C C T A C G G G C C A G A C C A G C G A
SEQ. ID. NO. 40	A C A A T G A T G C A A A G A A C T C A C A G C C
SEQ. ID. NO. 46	C T G A C C C T G G A G G G A G A C T T G G T G C
SEQ. ID. NO. 36	C T G A C C C T G G A G G G A G A C T T G G T G C
SEQ. ID. NO. 32	G C C C A A A A G A A G G G G G A C A T T A T C C
SEQ. ID. NO. 40	A G G A G T A T G C C C A T T C C A T A C G G G T
SEQ. ID. NO. 46	T G G G T G G G C T G T T C C C A G T G C A C C A
SEQ. ID. NO. 36	T G G G T G G G C T G T T C C C A G T G C A C C A
SEQ. ID. NO. 32	T T G G G G G G C T C T T T C C T A T T C A T T T
SEQ. ID. NO. 40	G G A T G G G G A C A T T A T T T T G G G G G G T
SEQ. ID. NO. 46	G A A G G G C G G C C C A G C A G A G G A C T G T
SEQ. ID. NO. 36	G A A G G G C G G C C C A G C A G A G G A C T G T
SEQ. ID. NO. 32	T G G A G T A G C A G C T A A A G A T C A A G A T
SEQ. ID. NO. 40	C T C T T C C C T G T C C A C G C A A A G G G A G
SEQ. ID. NO. 46	G G T C C T G T C A A T G A G C A C C G T G G C A
SEQ. ID. NO. 36	G G T C C T G T C A A T G A G C A C C G T G G C A
SEQ. ID. NO. 32	C T C A A A T C A A G G C C G G A G T C T G T G G
SEQ. ID. NO. 40	A G A G A G G G G T G C C T T G T G G G G A G C T
SEQ. ID. NO. 46	T C C A G C G C C T G G A G G C C A T G C T T T T
SEQ. ID. NO. 36	T C C A G C G C C T G G A G G C C A T G C T T T T
SEQ. ID. NO. 32	A A T G T A T C A G G T A T A A T T T C C G T G G

Figure 11a

SEQ. ID. NO. 40 G A A G A A G G A A A A G G G G A T T C A C A G A
SEQ. ID. NO. 46 T G C A C T G G A C C G C A T C A A C C G T G A C
SEQ. ID. NO. 36 T G C A C T G G A C C G C A T C A A C C G T G A C
SEQ. ID. NO. 32 G T T T C G C T G G T T A C A G G C T A T G A T A

SEQ. ID. NO. 40 C T G G A G G C C A T G C T T T A T G C A A T T G
SEQ. ID. NO. 46 C C G C A C C T G C T G C C T G G C G T G C G C C
SEQ. ID. NO. 36 C C G C A C C T G C T G C C T G G C G T G C G C C
SEQ. ID. NO. 32 T T T G C C A T A G A G G A G A T A A A C A G C A

SEQ. ID. NO. 40 A C C A G A T T A A C A A G G A C C C T G A T C T
SEQ. ID. NO. 46 T G G G T G C A C A C A T C C T C G A C A G T T G
SEQ. ID. NO. 36 T G G G T G C A C A C A T C C T C G A C A G T T G
SEQ. ID. NO. 32 G C C C A G C C C T T C T T C C C A A C T T G A C

SEQ. ID. NO. 40 C C T T T C C A A C A T C A C T C T G G G T G T C
SEQ. ID. NO. 46 C T C C A A G G A C A C A C A T G C G C T G G A G
SEQ. ID. NO. 36 C T C C A A G G A C A C A C A T G C G C T G G A G
SEQ. ID. NO. 32 G C T G G G A T A C A G G A T A T T T G A C A C T

SEQ. ID. NO. 40 C G C A T C C T C G A C A C G T G C T C T A G G G
SEQ. ID. NO. 46 C A G G C A C T G G A C T T T G T G C G T G C C T
SEQ. ID. NO. 36 C A G G C A C T G G A C T T T G T G C G T G C C T
SEQ. ID. NO. 32 T G C A A C A C C G T T T C T A A G G C C T T G G

SEQ. ID. NO. 40 A C A C C T A T G C T T T G G A G C A G T C T C T
SEQ. ID. NO. 46 C A C T C A G C C G T G G T G C T G A T G G C T C
SEQ. ID. NO. 36 C A C T C A G C C G T G G T G C T G A T G G C T C
SEQ. ID. NO. 32 A A G C C A C C C T G A G T T T T G T T G C T C A

SEQ. ID. NO. 40 A A C A T T C G T G C A G G C A T T A A T A G A G
SEQ. ID. NO. 46 A C G C C A C A T C T G C C C C G A C G G C T C T
SEQ. ID. NO. 36 A C G C C A C A T C T G C C C C G A C G G C T C T
SEQ. ID. NO. 32 A A A C A A A A T T G A T T C T T T G A A C C T T

SEQ. ID. NO. 40 A A A G A T G C T T C G G A T G T G A A G T G T G
SEQ. ID. NO. 46 T A T G C G A C C C A T G G T G A T G C T C C C A
SEQ. ID. NO. 36 T A T G C G A C C C A T G G T G A T G C T C C C A
SEQ. ID. NO. 32 G A T G A G T T C T G C A A C T G C T C A G A G C

Figure 11b

SEQ. ID. NO. 40 C T A A T G G A G A T C C A C C C A T T T T C A C
SEQ. ID. NO. 46 C T G C C A T C A C T G G T G T T A T T G G C G G
SEQ. ID. NO. 36 C T G C C A T C A C T G G T G T T A T T G G C G G
SEQ. ID. NO. 32 A C A T T C C C T C T A C G A T T G C T G T G G T

SEQ. ID. NO. 40 C A A G C C C G A C A A G A T T T C T G G C G T C
SEQ. ID. NO. 46 T T C C T A C A G T G A T G T C T C C A T C C A G
SEQ. ID. NO. 36 T T C C T A C A G T G A T G T C T C C A T C C A G
SEQ. ID. NO. 32 G G G A G C A A C T G G C T C A G G C G T C T C C

SEQ. ID. NO. 40 A T A G G T G C T G C A G C A A G C T C C G T G T
SEQ. ID. NO. 46 G T G G C C A A C C T C T T G A G G C T A T T T C
SEQ. ID. NO. 36 G T G G C C A A C C T C T T G A G G C T A T T T C
SEQ. ID. NO. 32 A C G G C A G T G G C A A A T C T G C T G G G G C

SEQ. ID. NO. 40 C C A T C A T G G T T G C T A A C A T T T T A A G
SEQ. ID. NO. 46 A G A T C C C A C A G A T T A G C T A C G C C T C
SEQ. ID. NO. 36 A G A T C C C A C A G A T T A G C T A C G C C T C
SEQ. ID. NO. 32 T C T T C T A C A T T C C C C A G G T C A G T T A

SEQ. ID. NO. 40 A C T T T T T A A G A T A C C T C A A A T C A G C
SEQ. ID. NO. 46 T A C C A G T G C C A A G C T G A G T G A C A A G
SEQ. ID. NO. 36 T A C C A G T G C C A A G C T G A G T G A C A A G
SEQ. ID. NO. 32 T G C C T C C T C C A G C A G A C T C C T C A G C

SEQ. ID. NO. 40 T A T G C A T C C A C A G C C C C A G A G C T A A
SEQ. ID. NO. 46 T C C C G C T A T G A C T A C T T T G C C C G C A
SEQ. ID. NO. 36 T C C C G C T A T G A C T A C T T T G C C C G C A
SEQ. ID. NO. 32 A A C A A G A A T C A A T T C A A G T C T T T C C

SEQ. ID. NO. 40 G T G A T A A C A C C A G G T A T G A C T T T T T
SEQ. ID. NO. 46 C A G T G C C T C C T G A C T T C T T C C A A G C
SEQ. ID. NO. 36 C A G T G C C T C C T G A C T T C T T C C A A G C
SEQ. ID. NO. 32 T C C G A A C C A T C C C C A A T G A T G A G C A

SEQ. ID. NO. 40 C T C T C G A G T G G T T C C G C C T G A C T C C
SEQ. ID. NO. 46 C A A G G C C A T G G C T G A G A T T C T C C G C
SEQ. ID. NO. 36 C A A G G C C A T G G C T G A G A T T C T C C G C
SEQ. ID. NO. 32 C C A G G C C A C T G C C A T G G C A G A C A T C

Figure 11c

SEQ. ID. NO. 40 T A C C A A G C C C A A G C C A T G G T G G A C A
SEQ. ID. NO. 46 T T C T T C A A C T G G A C C T A T G T G T C C A
SEQ. ID. NO. 36 T T C T T C A A C T G G A C C T A T G T G T C C A
SEQ. ID. NO. 32 A T C G A G T A T T T C C G C T G G A A C T G G G

SEQ. ID. NO. 40 T C G T G A C A G C A C T G G G A T G G A A T T A
SEQ. ID. NO. 46 C T G T G G C G T C T G A G G G C G A C T A T G G
SEQ. ID. NO. 36 C T G T G G C G T C T G A G G G C G A C T A T G G
SEQ. ID. NO. 32 T G G G C A C A A T T G C A G C T G A T G A C G A

SEQ. ID. NO. 40 T G T T T C G A C A C T G G C T T C T G A G G G G
SEQ. ID. NO. 46 C G A G A C A G G C A T T G A G G C C T T T G A G
SEQ. ID. NO. 36 C G A G A C A G G C A T T G A G G C C T T T G A G
SEQ. ID. NO. 32 C T A T G G G C G G C C G G G G A T T G A G A A A

SEQ. ID. NO. 40 A A C T A T G G T G A G A G C G G T G T G G A G G
SEQ. ID. NO. 46 C T A G A G G C T C G T G C C C G C A A C A T C T
SEQ. ID. NO. 36 C T A G A G G C T C G T G C C C G C A A C A T C T
SEQ. ID. NO. 32 T T C C G A G A G G A A G C T G A G G A A A G G G

SEQ. ID. NO. 40 C C T T C A C C C A G A T C T C G A G G G A G A T
SEQ. ID. NO. 46 G T G T G G C C A C C T C G G A G A A A G T G G G
SEQ. ID. NO. 36 G T G T G G C C A C C T C G G A G A A A G T G G G
SEQ. ID. NO. 32 A T A T C T G C A T C G A C T T C A G T G A A C T

SEQ. ID. NO. 40 T G G T G G T G T T T G C A T T G C T C A G T C A
SEQ. ID. NO. 46 C C G T G C C A T G A G C C G C G C G G C C T T T
SEQ. ID. NO. 36 C C G T G C C A T G A G C C G C G C G G C C T T T
SEQ. ID. NO. 32 C A T C T C C C A G T A C T C T G A T G A G G A A

SEQ. ID. NO. 40 C A G A A A A T C C C A C G T G A A C C A A G A C
SEQ. ID. NO. 46 G A G G G T G T G G T G C G A G C C C T G C T G C
SEQ. ID. NO. 36 G A G G G T G T G G T G C G A G C C C T G C T G C
SEQ. ID. NO. 32 G A G A T C C A G C A T G T G G T A G A G G T G A

SEQ. ID. NO. 40 C T G G A G A A T T T G A A A A A A T T A T C A A
SEQ. ID. NO. 46 A G A A G C C C A G T G C C C G C G T G G C T G T
SEQ. ID. NO. 36 A G A A G C C C A G T G C C C G C G T G G C T G T
SEQ. ID. NO. 32 T T C A A A A T T C C A C G G C C A A A G T C A T

Figure 11d

SEQ. ID. NO. 40 A C G C C T G C T A G A A A C A C C T A A T G C T
SEQ. ID. NO. 46 C C T G T T C A C C C G T T C T G A G G A T G C C
SEQ. ID. NO. 36 C C T G T T C A C C C G T T C T G A G G A T G C C
SEQ. ID. NO. 32 C G T G G T T T T C T C C A G T G G C C C A G A T

SEQ. ID. NO. 40 C G A G C A G T G A T T A T G T T T G C C A A T G
SEQ. ID. NO. 46 C G G G A G C T G C T T G C T G C C A G C C A G C
SEQ. ID. NO. 36 C G G G A G C T G C T T G C T G C C A G C C A G C
SEQ. ID. NO. 32 C T T G A G C C C C T C A T C A A G G A G A T T G

SEQ. ID. NO. 40 A G G A T G A C A T C A G G A G G A T A T T G G A
SEQ. ID. NO. 46 G C C T C A A T G C C A G C T T C A C C T G G G T
SEQ. ID. NO. 36 G C C T C A A T G C C A G C T T C A C C T G G G T
SEQ. ID. NO. 32 T C C G G C G C A A T A T C A C G G G C A A G A T

SEQ. ID. NO. 40 A G C A G C A A A A A A A C T A A A C C A A A G T
SEQ. ID. NO. 46 G G C C A G T G A T G G T T G G G G G G C C C T G
SEQ. ID. NO. 36 G G C C A G T G A T G G T T G G G G G G C C C T G
SEQ. ID. NO. 32 C T G G C T G G C C A G C G A G G C C T G G G C C

SEQ. ID. NO. 40 G G G C A T T T T C T C T G G A T T G G C T C A G
SEQ. ID. NO. 46 G A G A G T G T G G T G G C A G G C A G T G A G G
SEQ. ID. NO. 36 G A G A G T G T G G T G G C A G G C A G T G A G G
SEQ. ID. NO. 32 A G C T C C T C C C T G A T C G C C A T G C C T C

SEQ. ID. NO. 40 A T A G T T G G G G A T C C A A A A T A G C A C C
SEQ. ID. NO. 46 G G G C T G C T G A G G G T G C T A T C A C C A T
SEQ. ID. NO. 36 G G G C T G C T G A G G G T G C T A T C A C C A T
SEQ. ID. NO. 32 A G T A C T T C C A C G T G G T T G G C G G C A C

SEQ. ID. NO. 40 T G T C T A T C A G C A A G A G G A G A T T G C A
SEQ. ID. NO. 46 C G A G C T G G C C T C C T A C C C C A T C A G T
SEQ. ID. NO. 36 C G A G C T G G C C T C C T A C C C C A T C A G T
SEQ. ID. NO. 32 C A T T G G A T T C G C T C T G A A G G C T G G G

SEQ. ID. NO. 40 G A A G G G G C T G T G A C A A T T T T G C C C A
SEQ. ID. NO. 46 G A C T T T G C C T C C T A C T T C C A G A G C C
SEQ. ID. NO. 36 G A C T T T G C C T C C T A C T T C C A G A G C C
SEQ. ID. NO. 32 C A G A T C C C A G G C T T C C G G G A A T T C C

Figure 11e

SEQ. ID. NO. 40	A A C G A G C A T C A A T T G A T G G A T T T G A
SEQ. ID. NO. 46	T G G A C C C T T G G A A C A A C A G C C G G A A
SEQ. ID. NO. 36	T G G A C C C T T G G A A C A A C A G C C G G A A
SEQ. ID. NO. 32	T G A A G A A G G T C C A T C C C A G G A A G T C
SEQ. ID. NO. 40	T C G A T A C T T T A G A A G C C G A A C T C T T
SEQ. ID. NO. 46	C C C C T G G T T C C G T G A A T T C T G G G A G
SEQ. ID. NO. 36	C C C C T G G T T C C G T G A A T T C T G G G A G
SEQ. ID. NO. 32	T G T C C A C A A T G G T T T T G C C A A G G A G
SEQ. ID. NO. 40	G C C A A T A A T C G A A G A A A T G T G T G G T
SEQ. ID. NO. 46	C A G A G G T T C C G C T G C A G C T T C C G G C
SEQ. ID. NO. 36	C A G A G G T T C C G C T G C A G C T T C C G G C
SEQ. ID. NO. 32	T T T T G G G A A G A A A C A T T T A A C T G C C
SEQ. ID. NO. 40	T T G C A G A A T T C T G G G A G G A G A A T T T
SEQ. ID. NO. 46	A G C G A G A C T G C G C A G C C C A C T C T C T
SEQ. ID. NO. 36	A G C G A G A C T G C G C A G C C C A C T C T C T
SEQ. ID. NO. 32	A C C T C C A A G A A G G T G C A A A A G G A C C
SEQ. ID. NO. 40	T G G C T G C A A G T T A G G A T C A C A T G G G
SEQ. ID. NO. 46	C C G G G C T G T G C C C T T T G A G C A G G A G
SEQ. ID. NO. 36	C C G G G C T G T G C C C T T T G A G C A G G A G
SEQ. ID. NO. 32	T T T A C C T G T G G A C A C C T T T C T G A G A
SEQ. ID. NO. 40	A A A A G G A A C A G T C A T A T A A A G A A A T
SEQ. ID. NO. 46	T C C A A G A T C A T G T T T G T G G T C A A T G
SEQ. ID. NO. 36	T C C A A G A T C A T G T T T G T G G T C A A T G
SEQ. ID. NO. 32	G G T C A C G A A G A A A G T G G C G A C A G G T
SEQ. ID. NO. 40	G C A C A G G G C T G G A G C G A A T T G C T C G
SEQ. ID. NO. 46	C A G T G T A C G C C A T G G C C C A T G C G C T
SEQ. ID. NO. 36	C A G T G T A C G C C A T G G C C C A T G C G C T
SEQ. ID. NO. 32	T T A G C A A C A G C T C G A C A G C C T T C C G
SEQ. ID. NO. 40	G G A T T C A T C T T A T G A A C A G G A A G G A
SEQ. ID. NO. 46	C C A C A A C A T G C A C C G T G C C C T C T G C
SEQ. ID. NO. 36	C C A C A A C A T G C A C C G T G C C C T C T G C
SEQ. ID. NO. 32	A C C C C T C T G T A C A G G G G A T G A G A A C

Figure 11f

SEQ. ID. NO. 40 A A G G T C C A A T T T G T A A T T G A T G C T G
SEQ. ID. NO. 46 C C C A A C A C C A C C C G G C T C T G T G A C G
SEQ. ID. NO. 36 C C C A A C A C C A C C C G G C T C T G T G A C G
SEQ. ID. NO. 32 A T C A G C A G T G T C G A G A C C C C T T A C A

SEQ. ID. NO. 40 T A T A T T C C A T G G C T T A C G C C C T G C A
SEQ. ID. NO. 46 C G A T G C G G C C A G T T A A C G G G C G C C G
SEQ. ID. NO. 36 C G A T G C G G C C A G T T A A C G G G C G C C G
SEQ. ID. NO. 32 T A G A T T A C A C G C A T T T A C G G A T A T C

SEQ. ID. NO. 40 C A A T A T G C A C A A A G A T C T C T G C C C T
SEQ. ID. NO. 46 C C T C T A C A A G G A C T T T G T G C T C A A C
SEQ. ID. NO. 36 C C T C T A C A A G G A C T T T G T G C T C A A C
SEQ. ID. NO. 32 C T A C A A T G T G T A C T T A G C A G T C T A C

SEQ. ID. NO. 40 G G A T A C A T T G G C C T T T G T C C A C G A A
SEQ. ID. NO. 46 G T C A A G T T T G A T G C C C C C T T T C G C C
SEQ. ID. NO. 36 G T C A A G T T T G A T G C C C C C T T T C G C C
SEQ. ID. NO. 32 T C C A T T G C C C A C G C C T T G C A A G A T A

SEQ. ID. NO. 40 T G A G T A C C A T T G A T G G G A A A G A G C T
SEQ. ID. NO. 46 C A G C T G A C A C C C A C A A T G A G G T C C G
SEQ. ID. NO. 36 C A G C T G A C A C C C A C A A T G A G G T C C G
SEQ. ID. NO. 32 T A T A T A C C T G C T T A C C T G G G A G A G G

SEQ. ID. NO. 40 A C T T G G T T A T A T T C G G G C T G T A A A T
SEQ. ID. NO. 46 C T T T G A C C G C T T T G G T G A T G G T A T T
SEQ. ID. NO. 36 C T T T G A C C G C T T T G G T G A T G G T A T T
SEQ. ID. NO. 32 G C T C T T C A C C A A T G G C T C C T G T G C A

SEQ. ID. NO. 40 T T T A A T G G C A G T G C T G G C A C T C C T G
SEQ. ID. NO. 46 G G C C G C T A C A A C A T C T T C A C C T A T C
SEQ. ID. NO. 36 G G C C G C T A C A A C A T C T T C A C C T A T C
SEQ. ID. NO. 32 G A C A T C A A G A A A G T T G A G G C G T G G C

SEQ. ID. NO. 40 T C A C T T T T A A T G A A A A C G G A G A T G C
SEQ. ID. NO. 46 T G C G T G C A G G C A G T G G G C G C T A T C G
SEQ. ID. NO. 36 T G C G T G C A G G C A G T G G G C G C T A T C G
SEQ. ID. NO. 32 A G G T C C T G A A G C A C C T A C G G C A T C T

Figure 11g

SEQ. ID. NO. 40 T C C T G G A C G T T A T G A T A T C T T C C A G
SEQ. ID. NO. 46 C T A C C A G A A G G T G G G C T A C T G G G C A
SEQ. ID. NO. 36 C T A C C A G A A G G T G G G C T A C T G G G C A
SEQ. ID. NO. 32 A A A C T T T A C A A A C A A T A T G G G G G A G

SEQ. ID. NO. 40 T A T C A A A T A A C C A A C A A A A G C A C A G
SEQ. ID. NO. 46 G A A G G C T T G A C T C T G G A C A C C A G C C
SEQ. ID. NO. 36 G A A G G C T T G A C T C T G G A C A C C A G C C
SEQ. ID. NO. 32 C A G G T G A C C T T T G A T G A G T G T G G T G

SEQ. ID. NO. 40 A G T A C A A A G T C A T C G G C C A C T G G A C
SEQ. ID. NO. 46 T C A T C C C A T G G G C C T C A C C C T C A G C
SEQ. ID. NO. 36 T C A T C C C A T G G G C C T C A C C C T C A G C
SEQ. ID. NO. 32 A C C T G G T G G G G A A C T A T T C C A T C A T

SEQ. ID. NO. 40 C A A T C A G C T T C A T C T A A A A G T G G A A
SEQ. ID. NO. 46 C G G C C C C C T G C C C G C C T C T C G C T G C
SEQ. ID. NO. 36 C G G C C C C C T G C C C G C C T C T C G C T G C
SEQ. ID. NO. 32 C A A C T G G C A C C T C T C C C C A G A G G A T

SEQ. ID. NO. 40 G A C A T G C A G T G G G C T C A T A G A G A A C
SEQ. ID. NO. 46 A G T G A G C C C T G C C T C C A G A A T G A G G
SEQ. ID. NO. 36 A G T G A G C C C T G C C T C C A G A A T G A G G
SEQ. ID. NO. 32 G G C T C C A T C G T G T T T A A G G A A G T C G

SEQ. ID. NO. 40 A T A C T C A C C C G G C G T C T G T C T G C A G
SEQ. ID. NO. 46 T G A A G A G T G T G C A G C C G G G C G A A G T
SEQ. ID. NO. 36 T G A A G A G T G T G C A G C C G G G C G A A G T
SEQ. ID. NO. 32 G G T A T T A C A A C G T C T A T G C C A A G A A

SEQ. ID. NO. 40 C C T G C C G T G T A A G C C A G G G G A G A G G
SEQ. ID. NO. 46 C T G C T G C T G G C T C T G C A T T C C G T G C
SEQ. ID. NO. 36 C T G C T G C T G G C T C T G C A T T C C G T G C
SEQ. ID. NO. 32 G G G A G A A A G A C T C T T C A T C A A C G A G

SEQ. ID. NO. 40 A A G A A A A C G G T G A A A G G G G T C C C T T
SEQ. ID. NO. 46 C A G C C C T A T G A G T A C C G A T T G G A C G
SEQ. ID. NO. 36 C A G C C C T A T G A G T A C C G A T T G G A C G
SEQ. ID. NO. 32 G A G A A A A T C C T G T G G A G T G G G T T C T

Figure 11h

SEQ. ID. NO. 40	G C T G C T G G C A C T G T G A A C G C T G T G A
SEQ. ID. NO. 46	A A T T C A C T T G C G C T G A T T G T G G C C T
SEQ. ID. NO. 36	A A T T C A C T T G C G C T G A T T G T G G C C T
SEQ. ID. NO. 32	C C A G G G A G G T G C C C T T C T C C A A C T G

SEQ. ID. NO. 40	A G G T T A C A A C T A C C A G G T G G A T G A G
SEQ. ID. NO. 46	G G G C T A C T G G C C C A A T G C C A G C C T G
SEQ. ID. NO. 36	G G G C T A C T G G C C C A A T G C C A G C C T G
SEQ. ID. NO. 32	C A G C C G A G A C T G C C T G G C A G G G A C C

SEQ. ID. NO. 40	C T G T C C T G T G A A C T T T G C C C T C T G G
SEQ. ID. NO. 46	A C T G G C T G C T T C G A A C T G C C C C A G G
SEQ. ID. NO. 36	A C T G G C T G C T T C G A A C T G C C C C A G G
SEQ. ID. NO. 32	A G G A A A G G G A T C A T T G A G G G G G A G C

SEQ. ID. NO. 40	A T C A G A G A C C C A A C A T G A A C C G C A C
SEQ. ID. NO. 46	A G T A C A T C C G C T G G G G C G A T G C C T G
SEQ. ID. NO. 36	A G T A C A T C C G C T G G G G C G A T G C C T G
SEQ. ID. NO. 32	C C A C C T G C T G C T T T G A G T G T G T G G A

SEQ. ID. NO. 40	A G G C T G C C A G C T T A T C C C C A T C A T C
SEQ. ID. NO. 46	G G C T G T G G G A C C T G T C A C C A T C G C C
SEQ. ID. NO. 36	G G C T G T G G G A C C T G T C A C C A T C G C C
SEQ. ID. NO. 32	G T G T C C T G A T G G G G A G T A T A G T G A T

SEQ. ID. NO. 40	A A A T T G G A G T G G C A T T C T C C C T G G G
SEQ. ID. NO. 46	T G C C T C G G T G C C C T G G C C A C C C T C T
SEQ. ID. NO. 36	T G C C T C G G T G C C C T G G C C A C C C T C T
SEQ. ID. NO. 32	G A G A C A G A T G C C A G T G C C T G T A A C A

SEQ. ID. NO. 40	C T G T G G T G C C T G T G T T T G T T G C A A T
SEQ. ID. NO. 46	T T G T G C T G G G T G T C T T T G T G C G G C A
SEQ. ID. NO. 36	T T G T G C T G G G T G T C T T T G T G C G G C A
SEQ. ID. NO. 32	A G T G C C C A G A T G A C T T C T G G T C C A A

SEQ. ID. NO. 40	A T T G G G A A T C A T C G C C A C C A C C T T T
SEQ. ID. NO. 46	C A A T G C C A C A C C A G T G G T C A A G G C C
SEQ. ID. NO. 36	C A A T G C C A C A C C A G T G G T C A A G G C C
SEQ. ID. NO. 32	T G A G A A C C A C A C C T C C T G C T T C G A A

Figure 11i

SEQ. ID. NO. 40 G T G A T C G T G A C C T T T G T C C G C T A T A
SEQ. ID. NO. 46 T C A G G T C G G G A G C T C T G C T A C A T C C
SEQ. ID. NO. 36 T C A G G T C G G G A G C T C T G C T A C A T C C
SEQ. ID. NO. 32 C T G C C C C A G G A G T A C A T C C G C T G G G

SEQ. ID. NO. 40 A T G A C A C A C C T A T C G T G A G G G C T T C
SEQ. ID. NO. 46 T G C T G G G T G G T G T C T T C C T C T G C T A
SEQ. ID. NO. 36 T G C T G G G T G G T G T C T T C C T C T G C T A
SEQ. ID. NO. 32 G C G A T G C C T G G G C T G T G G G A C C T G T

SEQ. ID. NO. 40 A G G A C G C G A A C T T A G T T A C G T G C T C
SEQ. ID. NO. 46 C T G C A T G A C C T T C A T C T T C A T T G C C
SEQ. ID. NO. 36 C T G C A T G A C C T T C A T C T T C A T T G C C
SEQ. ID. NO. 32 C A C C A T C G C C T G C C T C G G T G C C C T G

SEQ. ID. NO. 40 C T A A C G G G G A T T T T T C T C T G T T A T T
SEQ. ID. NO. 46 A A G C C A T C C A C G G C A G T G T G T A C C T
SEQ. ID. NO. 36 A A G C C A T C C A C G G C A G T G T G T A C C T
SEQ. ID. NO. 32 G C C A C C C T G T T T G T G C T G G G T G T C T

SEQ. ID. NO. 40 C A A T C A C G T T T T T A A T G A T T G C A G C
SEQ. ID. NO. 46 T A C G G C G T C T T G G T T T G G G C A C T G C
SEQ. ID. NO. 36 T A C G G C G T C T T G G T T T G G G C A C T G C
SEQ. ID. NO. 32 T T G T G C G G C A C A A T G C C A C A C C A G T

SEQ. ID. NO. 40 A C C A G A T A C A A T C A T A T G C T C C T T C
SEQ. ID. NO. 46 C T T C T C T G T C T G C T A C T C A G C C C T G
SEQ. ID. NO. 36 C T T C T C T G T C T G C T A C T C A G C C C T G
SEQ. ID. NO. 32 G G T C A A G G C C T C A G G T C G G G A G C T C

SEQ. ID. NO. 40 C G A C G G G T C T T C C T A G G A C T T G G C A
SEQ. ID. NO. 46 C T C A C C A A G A C C A A C C G C A T T G C A C
SEQ. ID. NO. 36 C T C A C C A A G A C C A A C C G C A T T G C A C
SEQ. ID. NO. 32 T G C T A C A T C C T G C T G G G T G G T G T C T

SEQ. ID. NO. 40 T G T G T T T C A G C T A T G C A G C C C T T C T
SEQ. ID. NO. 46 G C A T C T T C G G T G G G G C C C G G G A G G G
SEQ. ID. NO. 36 G C A T C T T C G G T G G G G C C C G G G A G G G
SEQ. ID. NO. 32 T C C T C T G C T A C T G C A T G A C C T T C A T

Figure 11j

SEQ. ID. NO. 40 G A C C A A A A C A A A C C G T A T C C A C C G A
SEQ. ID. NO. 46 T G C C C A G C G G C C A C G C T T C A T C A G T
SEQ. ID. NO. 36 T G C C C A G C G G C C A C G C T T C A T C A G T
SEQ. ID. NO. 32 C T T C A T T G C C A A G C C A T C C A C G G C A

SEQ. ID. NO. 40 A T A T T T G A G C A G G G G A A G A A A T C T G
SEQ. ID. NO. 46 C C T G C C T C A C A G G T G G C C A T C T G C C
SEQ. ID. NO. 36 C C T G C C T C A C A G G T G G C C A T C T G C C
SEQ. ID. NO. 32 G T G T G T A C C T T A C G G C G T C T T G G T T

SEQ. ID. NO. 40 T C A C A G C G C C C A A G T T C A T T A G T C C
SEQ. ID. NO. 46 T G G C A C T T A T C T C G G G C C A G C T G C T
SEQ. ID. NO. 36 T G G C A C T T A T C T C G G G C C A G C T G C T
SEQ. ID. NO. 32 T G G G C A C T G C C T T C T C T G T C T G C T A

SEQ. ID. NO. 40 A G C A T C T C A G C T G G T G A T C A C C T T C
SEQ. ID. NO. 46 C A T C G T G G T C G C C T G G C T G G T G G T G
SEQ. ID. NO. 36 C A T C G T G G T C G C C T G G C T G G T G G T G
SEQ. ID. NO. 32 C T C A G C C C T G C T C A C C A A G A C C A A C

SEQ. ID. NO. 40 A G C C T C A T C T C C G T C C A G C T C C T T G
SEQ. ID. NO. 46 G A G G C A C C G G G C A C A G G C A A G G A G A
SEQ. ID. NO. 36 G A G G C A C C G G G C A C A G G C A A G G A G A
SEQ. ID. NO. 32 C G C A T T G C A C G C A T C T T C G G T G G G G

SEQ. ID. NO. 40 G A G T G T T T G T C T G G T T T G T T G T G G A
SEQ. ID. NO. 46 C A G C C C C C G A A C G G C G G G A G G T G G T
SEQ. ID. NO. 36 C A G C C C C C G A A C G G C G G G A G G T G G T
SEQ. ID. NO. 32 C C C G G G A G G G T G C C C A G C G G C C A C G

SEQ. ID. NO. 40 T C C C C C C C A C A T C A T C A T T G A C T A T
SEQ. ID. NO. 46 G A C A C T G C G C T G C A A C C A C C G C G A T
SEQ. ID. NO. 36 G A C A C T G C G C T G C A A C C A C C G C G A T
SEQ. ID. NO. 32 C T T C A T C A G T C C T G C C T C A C A G G T G

SEQ. ID. NO. 40 G G A G A G C A G C G G A C A C T A G A T C C A G
SEQ. ID. NO. 46 G C A A G T A T G T T G G G C T C G C T G G C C T
SEQ. ID. NO. 36 G C A A G T A T G T T G G G C T C G C T G G C C T
SEQ. ID. NO. 32 G C C A T C T G C C T G G C A C T T A T C T C G G

Figure 11k

SEQ. ID. NO. 40	A G A A G G C C A G G G G A G T G C T C A A G T G
SEQ. ID. NO. 46	A C A A T G T G C T C C T C A T C G C G C T C T G
SEQ. ID. NO. 36	A C A A T G T G C T C C T C A T C G C G C T C T G
SEQ. ID. NO. 32	G C C A G C T G C T C A T C G T G G T C G C C T G
SEQ. ID. NO. 40	T G A C A T T T C T G A T C T C T C A C T C A T T
SEQ. ID. NO. 46	C A C G C T T T A T G C C T T C A A G A C T C G C
SEQ. ID. NO. 36	C A C G C T T T A T G C C T T C A A G A C T C G C
SEQ. ID. NO. 32	G C T G G T G G T G G A G G C A C C G G G C A C A
SEQ. ID. NO. 40	T G T T C A C T T G G A T A C A G T A T C C T C T
SEQ. ID. NO. 46	A A G T G C C C C G A A A A C T T C A A C G A G G
SEQ. ID. NO. 36	A A G T G C C C C G A A A A C T T C A A C G A G G
SEQ. ID. NO. 32	G G C A A G G A G A C A G C C C C C G A A C G G C
SEQ. ID. NO. 40	T G A T G G T C A C T T G T A C T G T T T A T G C
SEQ. ID. NO. 46	C C A A G T T C A T T G G C T T C A C C A T G T A
SEQ. ID. NO. 36	C C A A G T T C A T T G G C T T C A C C A T G T A
SEQ. ID. NO. 32	G G G A G G T G G T G A C A C T G C G C T G C A A
SEQ. ID. NO. 40	C A T T A A A A C G A G A G G T G T C C C A G A G
SEQ. ID. NO. 46	C A C C A C C T G C A T C A T C T G G C T G G C A
SEQ. ID. NO. 36	C A C C A C C T G C A T C A T C T G G C T G G C A
SEQ. ID. NO. 32	C C A C C G C G A T G C A A G T A T G T T G G G C
SEQ. ID. NO. 40	A C T T T C A A T G A A G C C A A A C C T A T T G
SEQ. ID. NO. 46	T T C C T G C C C A T C T T C T A T G T C A C C T
SEQ. ID. NO. 36	T T C C T G C C C A T C T T C T A T G T C A C C T
SEQ. ID. NO. 32	T C G C T G G C C T A C A A T G T G C T C C T C A
SEQ. ID. NO. 40	G A T T T A C C A T G T A T A C C A C C T G C A T
SEQ. ID. NO. 46	C C A G T G A C T A C C G G G T A C A G A C C A C
SEQ. ID. NO. 36	C C A G T G A C T A C C G G G T A C A G A C C A C
SEQ. ID. NO. 32	T C G C G C T C T G C A C G C T T T A T G C C T T
SEQ. ID. NO. 40	C A T T T G G T T A G C T T T C A T C C C C A T C
SEQ. ID. NO. 46	C A C C A T G T G C G T G T C A G T C A G C C T C
SEQ. ID. NO. 36	C A C C A T G T G C G T G T C A G T C A G C C T C
SEQ. ID. NO. 32	C A A T A C T C G C A A G T G C C C C G A A A A C

Figure 11L

SEQ. ID. NO. 40 T T T T T T G G T A C A G C C C A G T C A G C A G
SEQ. ID. NO. 46 A G C G G C T C C G T G G T G C T T G G C T G C C
SEQ. ID. NO. 36 A G C G G C T C C G T G G T G C T T G G C T G C C
SEQ. ID. NO. 32 T T C A A C G A G G C C A A G T T C A T T G G C T

SEQ. ID. NO. 40 A A A A G A T G T A C A T C C A G A C A A C A A C
SEQ. ID. NO. 46 T C T T T G C G C C C A A G C T G C A C A T C A T
SEQ. ID. NO. 36 T C T T T G C G C C C A A G C T G C A C A T C A T
SEQ. ID. NO. 32 T C A C C A T G T A C A C C A C C T G C A T C A T

SEQ. ID. NO. 40 A C T T A C T G T C T C C A T G A G T T T A A G T
SEQ. ID. NO. 46 C C T C T T C C A G C C G C A G A A G A A C A C C
SEQ. ID. NO. 36 C C T C T T C C A G C C G C A G A A G A A C A C C
SEQ. ID. NO. 32 C T G G C T G G C A T T G T T G C C C A T C T T C

SEQ. ID. NO. 40 G C T T C A G T A T C T C T G G G C A T G C T C T
SEQ. ID. NO. 46 A T C G A G G A G G T G C G T T G C A G C A C C G
SEQ. ID. NO. 36 A T C G A G G A G G T G C G T T G C A G C A C C G
SEQ. ID. NO. 32 T A T G T C A C C T C C A G T G A C T A C C G G G

SEQ. ID. NO. 40 A T A T G C C C A A G G T T T A T A T T A T A A T
SEQ. ID. NO. 46 C A G C T C A C G C T T T C A A G G T G G C T G C
SEQ. ID. NO. 36 C A G C T C A C G C T T T C A A G G T G G C T G C
SEQ. ID. NO. 32 T A C A G A C C A C C A C C A T G T G C G T G T C

SEQ. ID. NO. 40 T T T T C A T C C A G A A C A G A A T A C C A T C
SEQ. ID. NO. 46 C C G G G C C A C G C T G C G C C G C A G C A A C
SEQ. ID. NO. 36 C C G G G C C A C G C T G C G C C G C A G C A A C
SEQ. ID. NO. 32 A G T C A G C C T C A G C G G C T C C G T G G T G

SEQ. ID. NO. 40 G A G G A G G T G C G T T G C A G C A C C G C A G
SEQ. ID. NO. 46 G T C T C C C G C A A G C G G T C C A G C A G C C
SEQ. ID. NO. 36 G T C T C C C G C A A G C G G T C C A G C A G C C
SEQ. ID. NO. 32 C T T G G C T G C C T C T T T G C G C C C A A G C

SEQ. ID. NO. 40 C T C A C G C T T T C A A G G T G G C T G C C C G
SEQ. ID. NO. 46 T T G G A G G C T C C A C G G G A T C C A C C C C
SEQ. ID. NO. 36 T T G G A G G C T C C A C G G G A T C C A C C C C
SEQ. ID. NO. 32 T G C A C A T C A T C C T C T T C C A G C C G C A

Figure 11m

SEQ. ID. NO. 40 G G C C A C G C T G C G C C G C A G C A A C G T C
SEQ. ID. NO. 46 C T C C T C C T C C A T C A G C A G C A A G A G C
SEQ. ID. NO. 36 C T C C T C C T C C A T C A G C A G C A A G A G C
SEQ. ID. NO. 32 G A A G A A C G T G G T T A G C C A C C G G G C A

SEQ. ID. NO. 40 T C C C G C A A G C G G T C C A G C A G C C T T G
SEQ. ID. NO. 46 A A C A G C G A A G A C C C A T T C C C A C A G C
SEQ. ID. NO. 36 A A C A G C G A A G A C C C A T T C C C A C A G C
SEQ. ID. NO. 32 C C C A C C A G C C G C T T T G G C A G T G C T G

SEQ. ID. NO. 40 G A G G C T C C A C G G G A T C C A C C C C C T C
SEQ. ID. NO. 46 C C G A G A G G C A G A A G C A G C A G C A G C C
SEQ. ID. NO. 36 C C G A G A G G C A G A A G C A G C A G C A G C C
SEQ. ID. NO. 32 C T G C C A G G G G C C A G C T C C A G C C T T G G

SEQ. ID. NO. 40 C T C C T C C A T C A G C A G C A A G A G C A A C
SEQ. ID. NO. 46 G C T G G C C C T A A C C C A G C A A G A G C A G
SEQ. ID. NO. 36 G C T G G C C C T A A C C C A G C A A G A G C A G
SEQ. ID. NO. 32 C C A A G G G T C T G G C T C C C A G T T T G T C

SEQ. ID. NO. 40 A G C G A A G A C C C A T T C C C A C A G C C C G
SEQ. ID. NO. 46 C A G C A G C A G C C C C T G A C C C T C C C A C
SEQ. ID. NO. 36 C A G C A G C A G C C C C T G A C C C T C C C A C
SEQ. ID. NO. 32 C C C A C T G T T T G C A A T G G C C G T G A G G

SEQ. ID. NO. 40 A G A G G C A G A A G C A G C A G C A G C C G C T
SEQ. ID. NO. 46 A G C A G C A A C G A T C T C A G C A G C A G C C
SEQ. ID. NO. 36 A G C A G C A A C G A T C T C A G C A G C A G C C
SEQ. ID. NO. 32 T G G T G G A C T C G A C A A C G T C A T C G C T

SEQ. ID. NO. 40 G G C C C T A A C C C A G C A A G A G C A G C A G
SEQ. ID. NO. 46 C A G A T G C A A G C A G A A G G T C A T C T T T
SEQ. ID. NO. 36 C A G A T G C A A G C A G A A G G T C A T C T T T
SEQ. ID. NO. 32 T A T G A C T C T G G A G T C C A T C A T G G C G

SEQ. ID. NO. 40 C A G C A G C C C C T G A C C C T C C C A C A G C
SEQ. ID. NO. 46 G G C A G C G G C A C G G T C A C C T T C T C A C
SEQ. ID. NO. 36 G G C A G C G G C A C G G T C A C C T T C T C A C
SEQ. ID. NO. 32 T G C T G C C T G A G C G A G G A G G C C A A G G

Figure 11n

SEQ. ID. NO. 40	A G C A A C G A T C T C A G C A G C A G C C C A G
SEQ. ID. NO. 46	T G A G C T T T G A T G A G C C T C A G A A G A A
SEQ. ID. NO. 36	T G A G C T T T G A T G A G C C T C A G A A G A A
SEQ. ID. NO. 32	A A G C C C G G C G G A T C A A C G A C G A G A T
SEQ. ID. NO. 40	A T G C A A G C A G A A G G T C A T C T T T G G C
SEQ. ID. NO. 46	C G C C A T G G C C C A C G G G A A T T C T A C G
SEQ. ID. NO. 36	C G C C A T G G C C C A C G G G A A T T C T A C G
SEQ. ID. NO. 32	C G A G C G G C A G C T C C G C A G G G A C A A G
SEQ. ID. NO. 40	A G C G G C A C G G T C A C C T T C T C A C T G A
SEQ. ID. NO. 46	C A C C A G A A C T C C C T G G A G G C C C A G A
SEQ. ID. NO. 36	C A C C A G A A C T C C C T G G A G G C C C A G A
SEQ. ID. NO. 32	C G G G A C G C C C G C C G G G A G C T C A A G C
SEQ. ID. NO. 40	G C T T T G A T G A G C C T C A G A A G A A C G C
SEQ. ID. NO. 46	A A A G C A G C G A T A C G C T G A C C C G A C A
SEQ. ID. NO. 36	A A A G C A G C G A T A C G C T G A C C C G A C A
SEQ. ID. NO. 32	T G C T G C T G C T C G G G A C A G G A G A G A G
SEQ. ID. NO. 40	C A T G G C C C A C G G G A A T T C T A C G C A C
SEQ. ID. NO. 46	C C A G C C A T T A C T C C C G C T G C A G T G C
SEQ. ID. NO. 36	C C A G C C A T T A C T C C C G C T G C A G T G C
SEQ. ID. NO. 32	T G G C A A G A G T A C G T T T A T C A A G C A G
SEQ. ID. NO. 40	C A G A A C T C C C T G G A G G C C C A G A A A A
SEQ. ID. NO. 46	G G G G A A A C G G A C T T A G A T C T G A C C G
SEQ. ID. NO. 36	G G G G A A A C G G A C T T A G A T C T G A C C G
SEQ. ID. NO. 32	A T G A G A A T C A T C C A T G G G T C A G G A T
SEQ. ID. NO. 40	G C A G C G A T A C G C T G A C C C G A C A C C A
SEQ. ID. NO. 46	T C C A G G A A A C A G G T C T G C A A G G A C C
SEQ. ID. NO. 36	T C C A G G A A A C A G G T C T G C A A G G A C C
SEQ. ID. NO. 32	A C T C T G A T G A A G A T A A A A G G G G C T T
SEQ. ID. NO. 40	G C C A T T A C T C C C G C T G C A G T G C G G G
SEQ. ID. NO. 46	T G T G G G T G G A G A C C A G C G G C C A G A G
SEQ. ID. NO. 36	T G T G G G T G G A G A C C A G C G G C C A G A G
SEQ. ID. NO. 32	C A C C A A G C T G G T G T A T C A G A A C A T C

Figure 11o

SEQ. ID. NO. 40	G A A A C G G A C T T A G A T C T G A C C G T C C
SEQ. ID. NO. 46	G T G G A G G A C C C T G A A G A G T T G T C C C
SEQ. ID. NO. 36	G T G G A G G A C C C T G A A G A G T T G T C C C
SEQ. ID. NO. 32	T T C A C G G C C A T G C A G G C C A T G A T C A

SEQ. ID. NO. 40	A G G A A A C A G G T C T G C A A G G A C C T G T
SEQ. ID. NO. 46	C A G C A C T T G T A G T G T C C A G T T C A C A
SEQ. ID. NO. 36	C A G C A C T T G T A G T G T C C A G T T C A C A
SEQ. ID. NO. 32	G A G C C A T G G A C A C A C T C A A G A T C C C

SEQ. ID. NO. 40	G G G T G G A G A C C A G C G G C C A G A G G T G
SEQ. ID. NO. 46	G A G C T T T G T C A T C A G T G G T G G A G G C
SEQ. ID. NO. 36	G A G C T T T G T C A T C A G T G G T G G A G G C
SEQ. ID. NO. 32	A T A C A A G T A T G A G C A C A A T A A G G C T

SEQ. ID. NO. 40	G A G G A C C C T G A A G A G T T G T C C C C A G
SEQ. ID. NO. 46	A G C A C T G T T A C A G A A A A C G T A G T G A
SEQ. ID. NO. 36	A G C A C T G T T A C A G A A A A C G T A G T G A
SEQ. ID. NO. 32	C A T G C A C A A T T A G T T C G A G A A G T T G

SEQ. ID. NO. 40	C A C T T G T A G T G T C C A G T T C A C A G A G
SEQ. ID. NO. 46	A T T C A G C G G C C G C C A T G A C T C T G G A
SEQ. ID. NO. 36	A T T C A A T G A C T C T G G A G T C C A T C A T
SEQ. ID. NO. 32	A T G T G G A G A A G G T G T C T G C T T T T G A

SEQ. ID. NO. 40	C T T T G T C A T C A G T G G T G G A G G C A G C
SEQ. ID. NO. 46	G T C C A T C A T G G C G T G C T G C C T G A G C
SEQ. ID. NO. 36	G G C G T G C T G C C T G A G C G A G G A G G C C
SEQ. ID. NO. 32	G A A T C C A T A T G T A G A T G C A A T A A A G

SEQ. ID. NO. 40	A C T G T T A C A G A A A A C G T A G T G A A T T
SEQ. ID. NO. 46	G A G G A G G C C A A G G A A G C C C G G C G G A
SEQ. ID. NO. 36	A A G G A A G C C C G G C G G A T C A A C G A C G
SEQ. ID. NO. 32	A G T T T A T G G A A T G A T C C T G G A A T C C

SEQ. ID. NO. 40	C A -
SEQ. ID. NO. 46	T C A A C G A C G A G A T C G A G C G G C A G C T
SEQ. ID. NO. 36	A G A T C G A G C G G C A G C T C C G C A G G G A
SEQ. ID. NO. 32	A G G A A T G C T A T G A T A G A C G A C G A G A

Figure 11p

SEQ. ID. NO. 40	- -
SEQ. ID. NO. 46	C C G C A G G G A C A A G C G G G A C G C C C G C
SEQ. ID. NO. 36	C A A G C G G G A C G C C C G C C G G G A G C T C
SEQ. ID. NO. 32	A T A T C A A T T A T C T G A C T C T A C C A A A
SEQ. ID. NO. 40	- - - - - - - - - - - - - - - A T G A C T C T G G
SEQ. ID. NO. 46	C G G G A G C T C A A G C T G C T G C T G C T C G
SEQ. ID. NO. 36	A A G C T G C T G C T G C T C G G G A C A G G A G
SEQ. ID. NO. 32	T A C T A T C T T A A T G A C T T G G A C C G C G
SEQ. ID. NO. 40	A G T C C A T C A T G G C G T G C T G C C T G A G
SEQ. ID. NO. 46	G G A C A G G A G A G A G T G G C A A G A G T A C
SEQ. ID. NO. 36	A G A G T G G C A A G A G T A C G T T T A T C A A
SEQ. ID. NO. 32	T A G C T G A C C C T G C C T A C C T G C C T A C
SEQ. ID. NO. 40	C G A G G A G G C C A A G G A A G C C C G G C G G
SEQ. ID. NO. 46	G T T T A T C A A G C A G A T G A G A A T C A T C
SEQ. ID. NO. 36	G C A G A T G A G A A T C A T C C A T G G G T C A
SEQ. ID. NO. 32	G C A A C A A G A T G T G C T T A G A G T T C G A
SEQ. ID. NO. 40	A T C A A C G A C G A G A T C G A G C G G C A G C
SEQ. ID. NO. 46	C A T G G G T C A G G A T A C T C T G A T G A A G
SEQ. ID. NO. 36	G G A T A C T C T G A T G A A G A T A A A A G G G
SEQ. ID. NO. 32	G T C C C C A C C A C A G G G A T C A T C G A A T
SEQ. ID. NO. 40	T C C G C A G G G A C A A G C G G G A C G C C C G
SEQ. ID. NO. 46	A T A A A A G G G G C T T C A C C A A G C T G G T
SEQ. ID. NO. 36	G C T T C A C C A A G C T G G T G T A T C A G A A
SEQ. ID. NO. 32	A C C C C T T T G A C T T A C A A A G T G T C A T
SEQ. ID. NO. 40	C C G G G A G C T C A A G C T G C T G C T G C T C
SEQ. ID. NO. 46	G T A T C A G A A C A T C T T C A C G G C C A T G
SEQ. ID. NO. 36	C A T C T T C A C G G C C A T G C A G G C C A T G
SEQ. ID. NO. 32	T T T C A G A A T G G T C G A T G T A G G G G G C
SEQ. ID. NO. 40	G G G A C A G G A G A G A G T G G C A A G A G T A
SEQ. ID. NO. 46	C A G G C C A T G A T C A G A G C C A T G G A C A
SEQ. ID. NO. 36	A T C A G A G C C A T G G A C A C A C T C A A G A
SEQ. ID. NO. 32	C A A A G G T C A G A G A G A A G A A A A T G G A

Figure 11q

SEQ. ID. NO. 40	C G T T T A T C A A G C A G A T G A G A A T C A T
SEQ. ID. NO. 46	C A C T C A A G A T C C C A T A C A A G T A T G A
SEQ. ID. NO. 36	T C C C A T A C A A G T A T G A G C A C A A T A A
SEQ. ID. NO. 32	T A C A C T G C T T T G A A A A T G T C A C C T C
SEQ. ID. NO. 40	C C A T G G G T C A G G A T A C T C T G A T G A A
SEQ. ID. NO. 46	G C A C A A T A A G G C T C A T G C A C A A T T A
SEQ. ID. NO. 36	G G C T C A T G C A C A A T T A G T T C G A G A A
SEQ. ID. NO. 32	T A T C A T G T T T C T A G T A G C G C T T A G T
SEQ. ID. NO. 40	G A T A A A A G G G G C T T C A C C A A G C T G G
SEQ. ID. NO. 46	G T T C G A G A A G T T G A T G T G G A G A A G G
SEQ. ID. NO. 36	G T T G A T G T G G A G A A G G T G T C T G C T T
SEQ. ID. NO. 32	G A A T A T G A T C A A G T T C T C G T G G A G T
SEQ. ID. NO. 40	T G T A T C A G A A C A T C T T C A C G G C C A T
SEQ. ID. NO. 46	T G T C T G C T T T T G A G A A T C C A T A T G T
SEQ. ID. NO. 36	T T G A G A A T C C A T A T G T A G A T G C A A T
SEQ. ID. NO. 32	C A G A C A A T G A G A A C C G A A T G G A G G A
SEQ. ID. NO. 40	G C A G G C C A T G A T C A G A G C C A T G G A C
SEQ. ID. NO. 46	A G A T G C A A T A A A G A G T T T A T G G A A T
SEQ. ID. NO. 36	A A A G A G T T T A T G G A A T G A T C C T G G A
SEQ. ID. NO. 32	A A G C A A G G C T C T C T T T A G A A C A A T T
SEQ. ID. NO. 40	A C A C T C A A G A T C C C A T A C A A G T A T G
SEQ. ID. NO. 46	G A T C C T G G A A T C C A G G A A T G C T A T G
SEQ. ID. NO. 36	A T C C A G G A A T G C T A T G A T A G A C G A C
SEQ. ID. NO. 32	A T C A C A T A C C C C T G G T T C C A G A A C T
SEQ. ID. NO. 40	A G C A C A A T A A G G C T C A T G C A C A A T T
SEQ. ID. NO. 46	A T A G A C G A C G A G A A T A T C A A T T A T C
SEQ. ID. NO. 36	G A G A A T A T C A A T T A T C T G A C T C T A C
SEQ. ID. NO. 32	C C T C G G T T A T T C T G T T C T T A A A C A A
SEQ. ID. NO. 40	A G T T C G A G A A G T T G A T G T G G A G A A G
SEQ. ID. NO. 46	T G A C T C T A C C A A A T A C T A T C T T A A T
SEQ. ID. NO. 36	C A A A T A C T A T C T T A A T G A C T T G G A C
SEQ. ID. NO. 32	G A A A G A T C T T C T A G A G G A G A A A A T C

Figure 11r

SEQ. ID. NO. 40 G T G T C T G C T T T T G A G A A T C C A T A T G
SEQ. ID. NO. 46 G A C T T G G A C C G C G T A G C T G A C C C T G
SEQ. ID. NO. 36 C G C G T A G C T G A C C C T G C C T A C C T G C
SEQ. ID. NO. 32 A T G T A T T C C C A T C T A G T C G A C T A C T

SEQ. ID. NO. 40 T A G A T G C A A T A A A G A G T T T A T G G A A
SEQ. ID. NO. 46 C C T A C C T G C C T A C G C A A C A A G A T G T
SEQ. ID. NO. 36 C T A C G C A A C A A G A T G T G C T T A G A G T
SEQ. ID. NO. 32 T C C C A G A A T A T G A T G G A C C C C A G A G

SEQ. ID. NO. 40 T G A T C C T G G A A T C C A G G A A T G C T A T
SEQ. ID. NO. 46 G C T T A G A G T T C G A G T C C C C A C C A C A
SEQ. ID. NO. 36 T C G A G T C C C C A C C A C A G G G A T C A T C
SEQ. ID. NO. 32 A G A T G C C C A G G C A G C C C G A G A A T T C

SEQ. ID. NO. 40 G A T A G A C G A C G A G A A T A T C A A T T A T
SEQ. ID. NO. 46 G G G A T C A T C G A A T A C C C C T T T G A C T
SEQ. ID. NO. 36 G A A T A C C C C T T T G A C T T A C A A A G T G
SEQ. ID. NO. 32 A T T C T G A A G A T G T T C G T G G A C C T G A

SEQ. ID. NO. 40 C T G A C T C T A C C A A A T A C T A T C T T A A
SEQ. ID. NO. 46 T A C A A A G T G T C A T T T T C A G A A T G G T
SEQ. ID. NO. 36 T C A T T T T C A G A A T G G T C G A T G T A G G
SEQ. ID. NO. 32 A C C C A G A C A G T G A C A A A A T T A T C T A

SEQ. ID. NO. 40 T G A C T T G G A C C G C G T A G C T G A C C C T
SEQ. ID. NO. 46 C G A T G T A G G G G G C C A A A G G T C A G A G
SEQ. ID. NO. 36 G G G C C A A A G G T C A G A G A G A A G A A A A
SEQ. ID. NO. 32 C T C C C A C T T C A C G T G C G C C A C A G A C

SEQ. ID. NO. 40 G C C T A C C T G C C T A C G C A A C A A G A T G
SEQ. ID. NO. 46 A G A A G A A A A T G G A T A C A C T G C T T T G
SEQ. ID. NO. 36 T G G A T A C A C T G C T T T G A A A A T G T C A
SEQ. ID. NO. 32 A C C G A G A A T A T C C G C T T T G T C T T T G

SEQ. ID. NO. 40 T G C T T A G A G T T C G A G T C C C C A C C A C
SEQ. ID. NO. 46 A A A A T G T C A C C T C T A T C A T G T T T C T
SEQ. ID. NO. 36 C C T C T A T C A T G T T T C T A G T A G C G C T
SEQ. ID. NO. 32 C T G C C G T C A A G G A C A C C A T C C T C C A

Figure 11s

SEQ. ID. NO. 40 A G G G A T C A T C G A A T A C C C C T T T G A C
SEQ. ID. NO. 46 A G T A G C G C T T A G T G A A T A T G A T C A A
SEQ. ID. NO. 36 T A G T G A A T A T G A T C A A G T T C T C G T G
SEQ. ID. NO. 32 G T T G A A C C T G A A G G A C T G C G G T C T G

SEQ. ID. NO. 40 T T A C A A A G T G T C A T T T T C A G A A T G G
SEQ. ID. NO. 46 G T T C T C G T G G A G T C A G A C A A T G A G A
SEQ. ID. NO. 36 G A G T C A G A C A A T G A G A A C C G A A T G G
SEQ. ID. NO. 32 T T C T A A

SEQ. ID. NO. 40 T C G A T G T A G G G G G C C A A A G G T C A G A
SEQ. ID. NO. 46 A C C G A A T G G A G G A A A G C A A G G C T C T
SEQ. ID. NO. 36 A G G A A A G C A A G G C T C T C T T T A G A A C
SEQ. ID. NO. 32

SEQ. ID. NO. 40 G A G A A G A A A A T G G A T A C A C T G C T T T
SEQ. ID. NO. 46 C T T T A G A A C A A T T A T C A C A T A C C C C
SEQ. ID. NO. 36 A A T T A T C A C A T A C C C C T G G T T C C A G
SEQ. ID. NO. 32

SEQ. ID. NO. 40 G A A A A T G T C A C C T C T A T C A T G T T T C
SEQ. ID. NO. 46 T G G T T C C A G A A C T C C T C G G T T A T T C
SEQ. ID. NO. 36 A A C T C C T C G G T T A T T C T G T T C T T A A
SEQ. ID. NO. 32

SEQ. ID. NO. 40 T A G T A G C G C T T A G T G A A T A T G A T C A
SEQ. ID. NO. 46 T G T T C T T A A A C A A G A A A G A T C T T C T
SEQ. ID. NO. 36 A C A A G A A A G A T C T T C T A G A G G A G A A
SEQ. ID. NO. 32

SEQ. ID. NO. 40 A G T T C T C G T G G A G T C A G A C A A T G A G
SEQ. ID. NO. 46 A G A G G A G A A A A T C A T G T A T T C C C A T
SEQ. ID. NO. 36 A A T C A T G T A T T C C C A T C T A G T C G A C
SEQ. ID. NO. 32

SEQ. ID. NO. 40 A A C C G A A T G G A G G A A A G C A A G G C T C
SEQ. ID. NO. 46 C T A G T C G A C T A C T T C C C A G A A T A T G
SEQ. ID. NO. 36 T A C T T C C C A G A A T A T G A T G G A C C C C
SEQ. ID. NO. 32

Figure 11t

SEQ. ID. NO. 40	T C T T T A G A A C A A T T A T C A C A T A C C C
SEQ. ID. NO. 46	A T G G A C C C C A G A G A G A T G C C C A G G C
SEQ. ID. NO. 36	A G A G A G A T G C C C A G G C A G C C C G A G A
SEQ. ID. NO. 32	
SEQ. ID. NO. 40	C T G G T T C C A G A A C T C C T C G G T T A T T
SEQ. ID. NO. 46	A G C C C G A G A A T T C A T T C T G A A G A T G
SEQ. ID. NO. 36	A T T C A T T C T G A A G A T G T T C G T G G A C
SEQ. ID. NO. 32	
SEQ. ID. NO. 40	C T G T T C T T A A A C A A G A A A G A T C T T C
SEQ. ID. NO. 46	T T C G T G G A C C T G A A C C C A G A C A G T G
SEQ. ID. NO. 36	C T G A A C C C A G A C A G T G A C A A A A T T A
SEQ. ID. NO. 32	
SEQ. ID. NO. 40	T A G A G G A G A A A A T C A T G T A T T C C C A
SEQ. ID. NO. 46	A C A A A A T T A T C T A C T C C C A C T T C A C
SEQ. ID. NO. 36	T C T A C T C C C A C T T C A C G T G C G C C A C
SEQ. ID. NO. 32	
SEQ. ID. NO. 40	T C T A G T C G A C T A C T T C C C A G A A T A T
SEQ. ID. NO. 46	G T G C G C C A C A G A C A C C G A G A A T A T C
SEQ. ID. NO. 36	A G A C A C C G A G A A T A T C C G C T T T G T C
SEQ. ID. NO. 32	
SEQ. ID. NO. 40	G A T G G A C C C C A G A G A G A T G C C C A G G
SEQ. ID. NO. 46	C G C T T T G T C T T T G C T G C C G T C A A G G
SEQ. ID. NO. 36	T T T G C T G C C G T C A A G G A C A C C A T C C
SEQ. ID. NO. 32	
SEQ. ID. NO. 40	C A G C C C G A G A A T T C A T T C T G A A G A T
SEQ. ID. NO. 46	A C A C C A T C C T C C A G T T G A A C C T G A A
SEQ. ID. NO. 36	T C C A G T T G A A C C T G A A G G A C T G C G G
SEQ. ID. NO. 32	
SEQ. ID. NO. 40	G T T C G T G G A C C T G A A C C C A G A C A G T
SEQ. ID. NO. 46	G G A C T G C G G T C T G T T C T A A T T G T G C
SEQ. ID. NO. 36	T C T G T T C T A A
SEQ. ID. NO. 32	

Figure 11u

SEQ. ID. NO. 40 G A C A A A A T T A T C T A C T C C C A C T T C A
SEQ. ID. NO. 46 C T C C T A G A C A C C C G C C C T G C C C T T C
SEQ. ID. NO. 36
SEQ. ID. NO. 32

SEQ. ID. NO. 40 C G T G C G C C A C A G A C A C C G A G A A T A T
SEQ. ID. NO. 46 C C T G G T
SEQ. ID. NO. 36
SEQ. ID. NO. 32

SEQ. ID. NO. 40 C C G C T T T G T C T T T G C T G C C G T C A A G
SEQ. ID. NO. 46
SEQ. ID. NO. 36
SEQ. ID. NO. 32

SEQ. ID. NO. 40 G A C A C C A T C C T C C A G T T G A A C C T G A
SEQ. ID. NO. 46
SEQ. ID. NO. 36
SEQ. ID. NO. 32

SEQ. ID. NO. 40 A G G A C T G C G G T C T G T T C T A A
SEQ. ID. NO. 46
SEQ. ID. NO. 36
SEQ. ID. NO. 32

Figure 11v

ClustalW Formatted Alignments

SEQ. ID. NO. 41 M V C E G K R S A S C P C F F L L T A K F Y W I L
SEQ. ID. NO. 47 M G S L L A L P A L L L L W G A V A E G P A K K V
SEQ. ID. NO. 37 M G S L L A L P A L L L L W G A V A E G P A K K V
SEQ. ID. NO. 33 M A F Y S C C W V L L A L T W H T S A Y G P D Q R

SEQ. ID. NO. 41 T M M Q R T H S Q E Y A H S I R V D G D I I L G G
SEQ. ID. NO. 47 L T L E G D L V L G G L F P V H Q K G G P A E D C
SEQ. ID. NO. 37 L T L E G D L V L G G L F P V H Q K G G P A E D C
SEQ. ID. NO. 33 A Q K K G D I I L G G L F P I H F G V A A K D Q D

SEQ. ID. NO. 41 L F P V H A K G E R G V P C G E L K K E K G I H R
SEQ. ID. NO. 47 G P V N E H R G I Q R L E A M L F A L D R I N R D
SEQ. ID. NO. 37 G P V N E H R G I Q R L E A M L F A L D R I N R D
SEQ. ID. NO. 33 L K S R P E S V E C I R Y N F R G F R W L Q A M I

SEQ. ID. NO. 41 L E A M L Y A I D Q I N K D P D L L S N I T L G V
SEQ. ID. NO. 47 P H L L P G V R L G A H I L D S C S K D T H A L E
SEQ. ID. NO. 37 P H L L P G V R L G A H I L D S C S K D T H A L E
SEQ. ID. NO. 33 F A I E E I N S S P A L L P N L T L G Y R I F D T

SEQ. ID. NO. 41 R I L D T C S R D T Y A L E Q S L T F V Q A L I E
SEQ. ID. NO. 47 Q A L D F V R A S L S R G A D G S R H I C P D G S
SEQ. ID. NO. 37 Q A L D F V R A S L S R G A D G S R H I C P D G S
SEQ. ID. NO. 33 C N T V S K A L E A T L S F V A Q N K I D S L N L

SEQ. ID. NO. 41 K D A S D V K C A N G D P P I F T K P D K I S G V
SEQ. ID. NO. 47 Y A T H G D A P T A I T G V I G G S Y S D V S I Q
SEQ. ID. NO. 37 Y A T H G D A P T A I T G V I G G S Y S D V S I Q
SEQ. ID. NO. 33 D E F C N C S E H I P S T I A V V G A T G S G V S

SEQ. ID. NO. 41 I G A A A S S V S I M V A N I L R L F K I P Q I S
SEQ. ID. NO. 47 V A N L L R L F Q I P Q I S Y A S T S A K L S D K
SEQ. ID. NO. 37 V A N L L R L F Q I P Q I S Y A S T S A K L S D K
SEQ. ID. NO. 33 T A V A N L L G L F Y I P Q V S Y A S S S R L L S

SEQ. ID. NO. 41 Y A S T A P E L S D N T R Y D F F S R V V P P D S
SEQ. ID. NO. 47 S R Y D Y F A R T V P P D F F Q A K A M A E I L R
SEQ. ID. NO. 37 S R Y D Y F A R T V P P D F F Q A K A M A E I L R
SEQ. ID. NO. 33 N K N Q F K S F L R T I P N D E H Q A T A M A D I

Figure 12a

SEQ. ID. NO. 41	Y Q A Q A M V D I V T A L G W N Y V S T L A S E G
SEQ. ID. NO. 47	F F N W T Y V S T V A S E G D Y G E T G I E A F E
SEQ. ID. NO. 37	F F N W T Y V S T V A S E G D Y G E T G I E A F E
SEQ. ID. NO. 33	I E Y F R W N W V G T I A A D D D Y G R P G I E K
SEQ. ID. NO. 41	N Y G E S G V E A F T Q I S R E I G G V C I A Q S
SEQ. ID. NO. 47	L E A R A R N I C V A T S E K V G R A M S R A A F
SEQ. ID. NO. 37	L E A R A R N I C V A T S E K V G R A M S R A A F
SEQ. ID. NO. 33	F R E E A E E R D I C I D F S E L I S Q Y S D E E
SEQ. ID. NO. 41	Q K I P R E P R P G E F E K I I K R L L E T P N A
SEQ. ID. NO. 47	E G V V R A L L Q K P S A R V A V L F T R S E D A
SEQ. ID. NO. 37	E G V V R A L L Q K P S A R V A V L F T R S E D A
SEQ. ID. NO. 33	E I Q H V V E V I Q N S T A K V I V V F S S G P D
SEQ. ID. NO. 41	R A V I M F A N E D D I R R I L E A A K K L N Q S
SEQ. ID. NO. 47	R E L L A A S Q R L N A S F T W V A S D G W G A L
SEQ. ID. NO. 37	R E L L A A S Q R L N A S F T W V A S D G W G A L
SEQ. ID. NO. 33	L E P L I K E I V R R N I T G K I W L A S E A W A
SEQ. ID. NO. 41	G H F L W I G S D S W G S K I A P V Y Q Q E E I A
SEQ. ID. NO. 47	E S V V A G S E G A A E G A I T I E L A S Y P I S
SEQ. ID. NO. 37	E S V V A G S E G A A E G A I T I E L A S Y P I S
SEQ. ID. NO. 33	S S S L I A M P Q Y F H V V G G T I G F A L K A G
SEQ. ID. NO. 41	E G A V T I L P K R A S I D G F D R Y F R S R T L
SEQ. ID. NO. 47	D F A S Y F Q S L D P W N N S R N P W F R E F W E
SEQ. ID. NO. 37	D F A S Y F Q S L D P W N N S R N P W F R E F W E
SEQ. ID. NO. 33	Q I P G F R E F L K K V H P R K S V H N G F A K E
SEQ. ID. NO. 41	A N N R R N V W F A E F W E E N F G C K L G S H G
SEQ. ID. NO. 47	Q R F R C S F R Q R D C A A H S L R A V P F E Q E
SEQ. ID. NO. 37	Q R F R C S F R Q R D C A A H S L R A V P F E Q E
SEQ. ID. NO. 33	F W E E T F N C H L Q E G A K G P L P V D T F L R
SEQ. ID. NO. 41	K R N S H I K K C T G L E R I A R D S S Y E Q E G
SEQ. ID. NO. 47	S K I M F V V N A V Y A M A H A L H N M H R A L C
SEQ. ID. NO. 37	S K I M F V V N A V Y A M A H A L H N M H R A L C
SEQ. ID. NO. 33	G H E E S G D R F S N S S T A F R P L C T G D E N

Figure 12b

SEQ. ID. NO. 41 K V Q F V I D A V Y S M A Y A L H N M H K D L C P
SEQ. ID. NO. 47 P N T T R L C D A M R P V N G R R L Y K D F V L N
SEQ. ID. NO. 37 P N T T R L C D A M R P V N G R R L Y K D F V L N
SEQ. ID. NO. 33 I S S V E T P Y I D Y T H L R I S Y N V Y L A V Y

SEQ. ID. NO. 41 G Y I G L C P R M S T I D G K E L L G Y I R A V N
SEQ. ID. NO. 47 V K F D A P F R P A D T H N E V R F D R F G D G I
SEQ. ID. NO. 37 V K F D A P F R P A D T H N E V R F D R F G D G I
SEQ. ID. NO. 33 S I A H A L Q D I Y T C L P G R G L F T N G S C A

SEQ. ID. NO. 41 F N G S A G T P V T F N E N G D A P G R Y D I F Q
SEQ. ID. NO. 47 G R Y N I F T Y L R A G S G R Y R Y Q K V G Y W A
SEQ. ID. NO. 37 G R Y N I F T Y L R A G S G R Y R Y Q K V G Y W A
SEQ. ID. NO. 33 D I K K V E A W Q V L K H L R H L N F T N N M G E

SEQ. ID. NO. 41 Y Q I T N K S T E Y K V I G H W T N Q L H L K V E
SEQ. ID. NO. 47 E G L T L D T S L I P W A S P S A G P L P A S R C
SEQ. ID. NO. 37 E G L T L D T S L I P W A S P S A G P L P A S R C
SEQ. ID. NO. 33 Q V T F D E C G D L V G N Y S I I N W H L S P E D

SEQ. ID. NO. 41 D M Q W A H R E H T H P A S V C S L P C K P G E R
SEQ. ID. NO. 47 S E P C L Q N E V K S V Q P G E V C C W L C I P C
SEQ. ID. NO. 37 S E P C L Q N E V K S V Q P G E V C C W L C I P C
SEQ. ID. NO. 33 G S I V F K E V G Y Y N V Y A K K G E R L F I N E

SEQ. ID. NO. 41 K K T V K G V P C C W H C E R C E G Y N Y Q V D E
SEQ. ID. NO. 47 Q P Y E Y R L D E F T C A D C G L G Y W P N A S L
SEQ. ID. NO. 37 Q P Y E Y R L D E F T C A D C G L G Y W P N A S L
SEQ. ID. NO. 33 E K I L W S G F S R E V P F S N C S R D C L A G T

SEQ. ID. NO. 41 L S C E L C P L D Q R P N M N R T G C Q L I P I I
SEQ. ID. NO. 47 T G C F E L P Q E Y I R W G D A W A V G P V T I A
SEQ. ID. NO. 37 T G C F E L P Q E Y I R W G D A W A V G P V T I A
SEQ. ID. NO. 33 R K G I I E G E P T C C F E C V E C P D G E Y S D

SEQ. ID. NO. 41 K L E W H S P W A V V P V F V A I L G I I A T T F
SEQ. ID. NO. 47 C L G A L A T L F V L G V F V R H N A T P V V K A
SEQ. ID. NO. 37 C L G A L A T L F V L G V F V R H N A T P V V K A
SEQ. ID. NO. 33 E T D A S A C N K C P D D F W S N E N H T S C F E

Figure 12c

SEQ. ID. NO. 41 V I V T F V R Y N D T P I V R A S G R E L S Y V L
SEQ. ID. NO. 47 S G R E L C Y I L L G G V F L C Y C M T F I F I A
SEQ. ID. NO. 37 S G R E L C Y I L L G G V F L C Y C M T F I F I A
SEQ. ID. NO. 33 L P Q E Y I R W G D A W A V G P V T I A C L G A L

SEQ. ID. NO. 41 L T G I F L C Y S I T F L M I A A P D T I I C S F
SEQ. ID. NO. 47 K P S T A V C T L R R L G L G T A F S V C Y S A L
SEQ. ID. NO. 37 K P S T A V C T L R R L G L G T A F S V C Y S A L
SEQ. ID. NO. 33 A T L F V L G V F V R H N A T P V V K A S G R E L

SEQ. ID. NO. 41 R R V F L G L G M C F S Y A A L L T K T N R I H R
SEQ. ID. NO. 47 L T K T N R I A R I F G G A R E G A Q R P R F I S
SEQ. ID. NO. 37 L T K T N R I A R I F G G A R E G A Q R P R F I S
SEQ. ID. NO. 33 C Y I L L G G V F L C Y C M T F I F I A K P S T A

SEQ. ID. NO. 41 I F E Q G K K S V T A P K F I S P A S Q L V I T F
SEQ. ID. NO. 47 P A S Q V A I C L A L I S G Q L L I V V A W L V V
SEQ. ID. NO. 37 P A S Q V A I C L A L I S G Q L L I V V A W L V V
SEQ. ID. NO. 33 V C T L R R L G L G T A F S V C Y S A L L T K T N

SEQ. ID. NO. 41 S L I S V Q L L G V F V W F V V D P P H I I I D Y
SEQ. ID. NO. 47 E A P G T G K E T A P E R R E V V T L R C N H R D
SEQ. ID. NO. 37 E A P G T G K E T A P E R R E V V T L R C N H R D
SEQ. ID. NO. 33 R I A R I F G G A R E G A Q R P R F I S P A S Q V

SEQ. ID. NO. 41 G E Q R T L D P E K A R G V L K C D I S D L S L I
SEQ. ID. NO. 47 A S M L G S L A Y N V L L I A L C T L Y A F K T R
SEQ. ID. NO. 37 A S M L G S L A Y N V L L I A L C T L Y A F K T R
SEQ. ID. NO. 33 A I C L A L I S G Q L L I V V A W L V V E A P G T

SEQ. ID. NO. 41 C S L G Y S I L L M V T C T V Y A I K T R G V P E
SEQ. ID. NO. 47 K C P E N F N E A K F I G F T M Y T T C I I W L A
SEQ. ID. NO. 37 K C P E N F N E A K F I G F T M Y T T C I I W L A
SEQ. ID. NO. 33 G K E T A P E R R E V V T L R C N H R D A S M L G

SEQ. ID. NO. 41 T F N E A K P I G F T M Y T T C I I W L A F I P I
SEQ. ID. NO. 47 F L P I F Y V T S S D Y R V Q T T T M C V S V S L
SEQ. ID. NO. 37 F L P I F Y V T S S D Y R V Q T T T M C V S V S L
SEQ. ID. NO. 33 S L A Y N V L L I A L C T L Y A F N T R K C P E N

Figure 12d

SEQ. ID. NO. 41	F F G T A Q S A E K M Y I Q T T T L T V S M S L S
SEQ. ID. NO. 47	S G S V V L G C L F A P K L H I I L F Q P Q K N T
SEQ. ID. NO. 37	S G S V V L G C L F A P K L H I I L F Q P Q K N T
SEQ. ID. NO. 33	F N E A K F I G F T M Y T T C I I W L A L L P I F

SEQ. ID. NO. 41	A S V S L G M L Y M P K V Y I I I F H P E Q N T I
SEQ. ID. NO. 47	I E E V R C S T A A H A F K V A A R A T L R R S N
SEQ. ID. NO. 37	I E E V R C S T A A H A F K V A A R A T L R R S N
SEQ. ID. NO. 33	Y V T S S D Y R V Q T T T M C V S V S L S G S V V

SEQ. ID. NO. 41	E E V R C S T A A H A F K V A A R A T L R R S N V
SEQ. ID. NO. 47	V S R K R S S S L G G S T G S T P S S S I S S K S
SEQ. ID. NO. 37	V S R K R S S S L G G S T G S T P S S S I S S K S
SEQ. ID. NO. 33	L G C L F A P K L H I I L F Q P Q K N V V S H R A

SEQ. ID. NO. 41	S R K R S S S L G G S T G S T P S S S I S S K S N
SEQ. ID. NO. 47	N S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q
SEQ. ID. NO. 37	N S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q
SEQ. ID. NO. 33	P T S R F G S A A A R A S S S L G Q G S G S Q F V

SEQ. ID. NO. 41	S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q Q
SEQ. ID. NO. 47	Q Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F
SEQ. ID. NO. 37	Q Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F
SEQ. ID. NO. 33	P T V C N G R E V V D S T T S S L M T L E S I M A

SEQ. ID. NO. 41	Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F G
SEQ. ID. NO. 47	G S G T V T F S L S F D E P Q K N A M A H G N S T
SEQ. ID. NO. 37	G S G T V T F S L S F D E P Q K N A M A H G N S T
SEQ. ID. NO. 33	C C L S E E A K E A R R I N D E I E R Q L R R D K

SEQ. ID. NO. 41	S G T V T F S L S F D E P Q K N A M A H G N S T H
SEQ. ID. NO. 47	H Q N S L E A Q K S S D T L T R H Q P L L P L Q C
SEQ. ID. NO. 37	H Q N S L E A Q K S S D T L T R H Q P L L P L Q C
SEQ. ID. NO. 33	R D A R R E L K L L L L G T G E S G K S T F I K Q

SEQ. ID. NO. 41	Q N S L E A Q K S S D T L T R H Q P L L P L Q C G
SEQ. ID. NO. 47	G E T D L D L T V Q E T G L Q G P V G G D Q R P E
SEQ. ID. NO. 37	G E T D L D L T V Q E T G L Q G P V G G D Q R P E
SEQ. ID. NO. 33	M R I I H G S G Y S D E D K R G F T K L V Y Q N I

Figure 12e

SEQ. ID. NO. 41 E T D L D L T V Q E T G L Q G P V G G D Q R P E V
SEQ. ID. NO. 47 V E D P E E L S P A L V V S S S Q S F V I S G G G
SEQ. ID. NO. 37 V E D P E E L S P A L V V S S S Q S F V I S G G G
SEQ. ID. NO. 33 F T A M Q A M I R A M D T L K I P Y K Y E H N K A

SEQ. ID. NO. 41 E D P E E L S P A L V V S S S Q S F V I S G G G S
SEQ. ID. NO. 47 S T V T E N V V N S A A A M T L E S I M A C C L S
SEQ. ID. NO. 37 S T V T E N V V N S M T L E S I M A C C L S E E A
SEQ. ID. NO. 33 H A Q L V R E V D V E K V S A F E N P Y V D A I K

SEQ. ID. NO. 41 T V T E N V V N S M T L E S I M A C C L S E E A K
SEQ. ID. NO. 47 E E A K E A R R I N D E I E R Q L R R D K R D A R
SEQ. ID. NO. 37 K E A R R I N D E I E R Q L R R D K R D A R R E L
SEQ. ID. NO. 33 S L W N D P G I Q E C Y D R R R E Y Q L S D S T K

SEQ. ID. NO. 41 E A R R I N D E I E R Q L R R D K R D A R R E L K
SEQ. ID. NO. 47 R E L K L L L L G T G E S G K S T F I K Q M R I I
SEQ. ID. NO. 37 K L L L L G T G E S G K S T F I K Q M R I I H G S
SEQ. ID. NO. 33 Y Y L N D L D R V A D P A Y L P T Q Q D V L R V R

SEQ. ID. NO. 41 L L L L G T G E S G K S T F I K Q M R I I H G S G
SEQ. ID. NO. 47 H G S G Y S D E D K R G F T K L V Y Q N I F T A M
SEQ. ID. NO. 37 G Y S D E D K R G F T K L V Y Q N I F T A M Q A M
SEQ. ID. NO. 33 V P T T G I I E Y P F D L Q S V I F R M V D V G G

SEQ. ID. NO. 41 Y S D E D K R G F T K L V Y Q N I F T A M Q A M I
SEQ. ID. NO. 47 Q A M I R A M D T L K I P Y K Y E H N K A H A Q L
SEQ. ID. NO. 37 I R A M D T L K I P Y K Y E H N K A H A Q L V R E
SEQ. ID. NO. 33 Q R S E R R K W I H C F E N V T S I M F L V A L S

SEQ. ID. NO. 41 R A M D T L K I P Y K Y E H N K A H A Q L V R E V
SEQ. ID. NO. 47 V R E V D V E K V S A F E N P Y V D A I K S L W N
SEQ. ID. NO. 37 V D V E K V S A F E N P Y V D A I K S L W N D P G
SEQ. ID. NO. 33 E Y D Q V L V E S D N E N R M E E S K A L F R T I

SEQ. ID. NO. 41 D V E K V S A F E N P Y V D A I K S L W N D P G I
SEQ. ID. NO. 47 D P G I Q E C Y D R R R E Y Q L S D S T K Y Y L N
SEQ. ID. NO. 37 I Q E C Y D R R R E Y Q L S D S T K Y Y L N D L D
SEQ. ID. NO. 33 I T Y P W F Q N S S V I L F L N K K D L L E E K I

Figure 12f

```
SEQ. ID. NO. 41  Q E C Y D R R R E Y Q L S D S T K Y Y L N D L D R
SEQ. ID. NO. 47  D L D R V A D P A Y L P T Q Q D V L R V R V P T T
SEQ. ID. NO. 37  R V A D P A Y L P T Q Q D V L R V R V P T T G I I
SEQ. ID. NO. 33  M Y S H L V D Y F P E Y D G P Q R D A Q A A R E F

SEQ. ID. NO. 41  V A D P A Y L P T Q Q D V L R V R V P T T G I I E
SEQ. ID. NO. 47  G I I E Y P F D L Q S V I F R M V D V G G Q R S E
SEQ. ID. NO. 37  E Y P F D L Q S V I F R M V D V G G Q R S E R R K
SEQ. ID. NO. 33  I L K M F V D L N P D S D K I I Y S H F T C A T D

SEQ. ID. NO. 41  Y P F D L Q S V I F R M V D V G G Q R S E R R K W
SEQ. ID. NO. 47  R R K W I H C F E N V T S I M F L V A L S E Y D Q
SEQ. ID. NO. 37  W I H C F E N V T S I M F L V A L S E Y D Q V L V
SEQ. ID. NO. 33  T E N I R F V F A A V K D T I L Q L N L K D C G L

SEQ. ID. NO. 41  I H C F E N V T S I M F L V A L S E Y D Q V L V E
SEQ. ID. NO. 47  V L V E S D N E N R M E E S K A L F R T I I T Y P
SEQ. ID. NO. 37  E S D N E N R M E E S K A L F R T I I T Y P W F Q
SEQ. ID. NO. 33  F

SEQ. ID. NO. 41  S D N E N R M E E S K A L F R T I I T Y P W F Q N
SEQ. ID. NO. 47  W F Q N S S V I L F L N K K D L L E E K I M Y S H
SEQ. ID. NO. 37  N S S V I L F L N K K D L L E E K I M Y S H L V D
SEQ. ID. NO. 33

SEQ. ID. NO. 41  S S V I L F L N K K D L L E E K I M Y S H L V D Y
SEQ. ID. NO. 47  L V D Y F P E Y D G P Q R D A Q A A R E F I L K M
SEQ. ID. NO. 37  Y F P E Y D G P Q R D A Q A A R E F I L K M F V D
SEQ. ID. NO. 33

SEQ. ID. NO. 41  F P E Y D G P Q R D A Q A A R E F I L K M F V D L
SEQ. ID. NO. 47  F V D L N P D S D K I I Y S H F T C A T D T E N I
SEQ. ID. NO. 37  L N P D S D K I I Y S H F T C A T D T E N I R F V
SEQ. ID. NO. 33

SEQ. ID. NO. 41  N P D S D K I I Y S H F T C A T D T E N I R F V F
SEQ. ID. NO. 47  R F V F A A V K D T I L Q L N L K D C G L F
SEQ. ID. NO. 37  F A A V K D T I L Q L N L K D C G L F
SEQ. ID. NO. 33
```

Figure 12g

SEQ. ID. NO. 41	A A V K D T I L Q L N L K D C G L F
SEQ. ID. NO. 47	
SEQ. ID. NO. 37	
SEQ. ID. NO. 33	

Figure 12h

ClustalW Formatted Alignments

SEQ. ID. NO. 44 A T G T T G C T G C T G C T G C T A C T G G C G C
SEQ. ID. NO. 42 A T G G C T T C C C C G C G G A G C T C C G G G C

SEQ. ID. NO. 44 C A C T C T T C C T C C G C C C C C C G G G C G C
SEQ. ID. NO. 42 A G C C C G G G C C G C C G C C G C C G C C G C C

SEQ. ID. NO. 44 G G G C G G G G C G C A G A C C C C C A A C G C C
SEQ. ID. NO. 42 A C C G C C G C C C G C G C G C C T G C T A C T G

SEQ. ID. NO. 44 A C C T C A G A A G G T T G C C A G A T C A T A C
SEQ. ID. NO. 42 C T A C T G C T G C T G C C G C T G C T G C T G C

SEQ. ID. NO. 44 A C C C G C C C T G G G A A G G G G G C A T C A G
SEQ. ID. NO. 42 C T C T G G C G C C C G G G G C C T G G G G C T G

SEQ. ID. NO. 44 G T A C C G G G G C C T G A C T C G G G A C C A G
SEQ. ID. NO. 42 G G C G C G G G G C G C C C C C C G G C C G C C G

SEQ. ID. NO. 44 G T G A A G G C T A T C A A C T T C C T G C C A G
SEQ. ID. NO. 42 C C C A G C A G C C C G C C G C T C T C C A T C A

SEQ. ID. NO. 44 T G G A C T A T G A G A T T G A G T A T G T G T G
SEQ. ID. NO. 42 T G G G C C T C A T G C C G C T C A C C A A G G A

SEQ. ID. NO. 44 C C G G G G G G A G C G C G A G G T G G T G G G G
SEQ. ID. NO. 42 G G T G G C C A A G G G C A G C A T C G G G C G C

SEQ. ID. NO. 44 C C C A A G G T C C G C A A G T G C C T G G C C A
SEQ. ID. NO. 42 G G T G T G C T C C C C G C C G T G G A A C T G G

SEQ. ID. NO. 44 A C G G C T C C T G G A C A G A T A T G G A C A C
SEQ. ID. NO. 42 C C A T C G A G C A G A T C C G C A A C G A G T C

SEQ. ID. NO. 44 A C C C A G C C G C T G T G T C C G A A T C T G C
SEQ. ID. NO. 42 A C T C C T G C G C C C T T A C T T C C T C G A C

Figure 13a

SEQ. ID. NO. 44 T C C A A G T C T T A T T T G A C C C T G G A A A
SEQ. ID. NO. 42 C T G C G G C T C T A T G A C A C G G A G T G C G

SEQ. ID. NO. 44 A T G G A A G G T T T T C C T G A C G G G T G G
SEQ. ID. NO. 42 A C A A C G C A A A A G G G T T G A A A G C C T T

SEQ. ID. NO. 44 G G A C C T C C C A G C T C T G G A C G G A G C C
SEQ. ID. NO. 42 C T A C G A T G C A A T A A A A T A C G G G C C G

SEQ. ID. NO. 44 C G G G T G G A T T T C C G G T G T G A C C C C G
SEQ. ID. NO. 42 A A C C A C T T G A T G G T G T T T G G A G G C G

SEQ. ID. NO. 44 A C T T C C A T C T G G T G G G C A G C T C C C G
SEQ. ID. NO. 42 T C T G T C C A T C C G T C A C A T C C A T C A T

SEQ. ID. NO. 44 G A G C A T C T G T A G T C A G G G C C A G T G G
SEQ. ID. NO. 42 T G C A G A G T C C C T C C A A G G C T G G A A T

SEQ. ID. NO. 44 A G C A C C C C C A A G C C C C A C T G C C A G G
SEQ. ID. NO. 42 C T G G T G C A G C T T T C T T T T G C T G C A A

SEQ. ID. NO. 44 T G A A T C G A A C G C C A C A C T C A G A A C G
SEQ. ID. NO. 42 C C A C G C C T G T T C T A G C C G A T A A G A A

SEQ. ID. NO. 44 G C G C G C A G T G T A C A T C G G G G C A C T G
SEQ. ID. NO. 42 A A A A T A C C C T T A T T T C T T T C G G A C C

SEQ. ID. NO. 44 T T T C C C A T G A G C G G G G G C T G G C C A G
SEQ. ID. NO. 42 G T C C C A T C A G A C A A T G C G G T G A A T C

SEQ. ID. NO. 44 G G G G C C A G G C C T G C C A G C C C G C G G T
SEQ. ID. NO. 42 C A G C C A T T C T G A A G T T G C T C A A G C A

SEQ. ID. NO. 44 G G A G A T G G C G C T G G A G G A C G T G A A T
SEQ. ID. NO. 42 C T A C C A G T G G A A G C G C G T G G G C A C G

SEQ. ID. NO. 44 A G C C G C A G G G A C A T C C T G C C G G A C T
SEQ. ID. NO. 42 C T G A C G C A A G A C G T T C A G A G G T T C T

Figure 13b

SEQ. ID. NO. 44 A T G A G C T C A A G C T C A T C C A C C A C G A
SEQ. ID. NO. 42 C T G A G G T G C G G A A T G A C C T G A C T G G

SEQ. ID. NO. 44 C A G C A A G T G T G A T C C A G G C C A A G C C
SEQ. ID. NO. 42 A G T T C T G T A T G G C G A G G A C A T T G A G

SEQ. ID. NO. 44 A C C A A G T A C C T A T A T G A G C T G C T C T
SEQ. ID. NO. 42 A T T T C A G A C A C C G A G A G C T T C T C C A

SEQ. ID. NO. 44 A C A A C G A C C C T A T C A A G A T C A T C C T
SEQ. ID. NO. 42 A C G A T C C C T G T A C C A G T G T C A A A A A

SEQ. ID. NO. 44 T A T G C C T G G C T G C A G C T C T G T C T C C
SEQ. ID. NO. 42 G C T G A A G G G G A A T G A T G T G C G G A T C

SEQ. ID. NO. 44 A C G C T G G T G G C T G A G G C T G C T A G G A
SEQ. ID. NO. 42 A T C C T T G G C C A G T T T G A C C A G A A T A

SEQ. ID. NO. 44 T G T G G A A C C T C A T T G T G C T T T C C T A
SEQ. ID. NO. 42 T G G C A G C A A A A G T G T T C T G T T G T G C

SEQ. ID. NO. 44 T G G C T C C A G C T C A C C A G C C C T G T C A
SEQ. ID. NO. 42 A T A C G A G G A G A A C A T G T A T G G T A G T

SEQ. ID. NO. 44 A A C C G G C A G C G T T T C C C C A C T T T C T
SEQ. ID. NO. 42 A A A T A T C A G T G G A T C A T T C C G G G C T

SEQ. ID. NO. 44 T C C G A A C G C A C C C A T C A G C C A C A C T
SEQ. ID. NO. 42 G G T A C G A G C C T T C T T G G T G G G A G C A

SEQ. ID. NO. 44 C C A C A A C C C T A C C C G C G T G A A A C T C
SEQ. ID. NO. 42 G G T G C A C A C G G A A G C C A A C T C A T C C

SEQ. ID. NO. 44 T T T G A A A A G T G G G G C T G G A A G A A G A
SEQ. ID. NO. 42 C G C T G C C T C C G G A A G A A T C T G C T T G

SEQ. ID. NO. 44 T T G C T A C C A T C C A G C A G A C C A C T G A
SEQ. ID. NO. 42 C T G C C A T G G A G G G C T A C A T T G G C G T

Figure 13c

SEQ. ID. NO. 44	G G T C T T C A C T T C G A C T C T G G A C G A C
SEQ. ID. NO. 42	G G A T T T C G A G C C C C T G A G C T C C A A G
SEQ. ID. NO. 44	C T G G A G G A A C G A G T G A A G G A G G C T G
SEQ. ID. NO. 42	C A G A T C A A G A C C A T C T C A G G A A A G A
SEQ. ID. NO. 44	G A A T T G A G A T T A C T T T C C G C C A G A G
SEQ. ID. NO. 42	C T C C A C A G C A G T A T G A G A G A G A G T A
SEQ. ID. NO. 44	T T T C T T C T C A G A T C C A G C T G T G C C C
SEQ. ID. NO. 42	C A A C A A C A A G C G G T C A G G C G T G G G G
SEQ. ID. NO. 44	G T C A A A A A C C T G A A G C G C C A G G A T G
SEQ. ID. NO. 42	C C C A G C A A G T T C C A C G G G T A C G C C T
SEQ. ID. NO. 44	C C C G A A T C A T C G T G G G A C T T T T C T A
SEQ. ID. NO. 42	A C G A T G G C A T C T G G G T C A T C G C C A A
SEQ. ID. NO. 44	T G A G A C T G A A G C C C G G A A A G T T T T T
SEQ. ID. NO. 42	G A C A C T G C A G A G G G C C A T G G A G A C A
SEQ. ID. NO. 44	T G T G A G G T G T A C A A G G A G C G T C T C T
SEQ. ID. NO. 42	C T G C A T G C C A G C A G C C G G C A C C A G C
SEQ. ID. NO. 44	T T G G G A A G A A G T A C G T C T G G T T C C T
SEQ. ID. NO. 42	G G A T C C A G G A C T T C A A C T A C A C G G A
SEQ. ID. NO. 44	C A T T G G G T G G T A T G C T G A C A A T T G G
SEQ. ID. NO. 42	C C A C A C G C T G G G C A G G A T C A T C C T C
SEQ. ID. NO. 44	T T C A A G A T C T A C G A C C C T T C T A T C A
SEQ. ID. NO. 42	A A T G C C A T G A A C G A G A C C A A C T T C T
SEQ. ID. NO. 44	A C T G C A C A G T G G A T G A G A T G A C T G A
SEQ. ID. NO. 42	T C G G G G T C A C G G G T C A A G T T G T A T T
SEQ. ID. NO. 44	G G C G G T G G A G G G C C A C A T C A C A A C T
SEQ. ID. NO. 42	C C G G A A T G G G G A G A G A A T G G G G A C C

Figure 13d

SEQ. ID. NO. 44	G A G A T T G T C A T G C T G A A T C C T G C C A
SEQ. ID. NO. 42	A T T A A A T T T A C T C A A T T T C A A G A C A
SEQ. ID. NO. 44	A T A C C C G C A G C A T T T C C A A C A T G A C
SEQ. ID. NO. 42	G C A G G G A G G T G A A G G T G G G A G A G T A
SEQ. ID. NO. 44	A T C C C A G G A A T T T G T G G A G A A A C T A
SEQ. ID. NO. 42	C A A C G C T G T G G C C G A C A C A C T G G A G
SEQ. ID. NO. 44	A C C A A G C G A C T G A A A A G A C A C C C T G
SEQ. ID. NO. 42	A T C A T C A A T G A C A C C A T C A G G T T C C
SEQ. ID. NO. 44	A G G A G A C A G G A G G C T T C C A G G A G G C
SEQ. ID. NO. 42	A A G G A T C C G A A C C A C C A A A A G A C A A
SEQ. ID. NO. 44	A C C G C T G G C C T A T G A T G C C A T C T G G
SEQ. ID. NO. 42	G A C C A T C A T C C T G G A G C A G C T G C G G
SEQ. ID. NO. 44	G C C T T G G C A C T G G C C C T G A A C A A G A
SEQ. ID. NO. 42	A A G A T C T C C C T A C C T C T C T A C A G C A
SEQ. ID. NO. 44	C A T C T G G A G G A G G C G G C C G T T C T G G
SEQ. ID. NO. 42	T C C T C T C T G C C C T C A C C A T C C T C G G
SEQ. ID. NO. 44	T G T G C G C C T G G A G G A C T T C A A C T A C
SEQ. ID. NO. 42	G A T G A T C A T G G C C A G T G C T T T T C T C
SEQ. ID. NO. 44	A A C A A C C A G A C C A T T A C C G A C C A A A
SEQ. ID. NO. 42	T T C T T C A A C A T C A A G A A C C G G A A T C
SEQ. ID. NO. 44	T C T A C C G G G C A A T G A A C T C T T C G T C
SEQ. ID. NO. 42	A G A A G C T C A T A A A G A T G T C G A G T C C
SEQ. ID. NO. 44	C T T T G A G G G T G T C T C T G G C C A T G T G
SEQ. ID. NO. 42	A T A C A T G A A C A A C C T T A T C A T C C T T
SEQ. ID. NO. 44	G T G T T T G A T G C C A G C G G C T C T C G G A
SEQ. ID. NO. 42	G G A G G G A T G C T C T C C T A T G C T T C C A

Figure 13e

SEQ. ID. NO. 44 T G G C A T G G A C G C T T A T C G A G C A G C T
SEQ. ID. NO. 42 T A T T T C T C T T T G G C C T T G A T G G A T C

SEQ. ID. NO. 44 T C A G G G T G G C A G C T A C A A G A A G A T T
SEQ. ID. NO. 42 C T T T G T C T C T G A A A A G A C C T T T G A A

SEQ. ID. NO. 44 G G C T A C T A T G A C A G C A C C A A G G A T G
SEQ. ID. NO. 42 A C A C T T T G C A C C G T C A G G A C C T G G A

SEQ. ID. NO. 44 A T C T T T C C T G G T C C A A A A C A G A T A A
SEQ. ID. NO. 42 T T C T C A C C G T G G G C T A C A C G A C C G C

SEQ. ID. NO. 44 A T G G A T T G G A G G G T C C C C C C C A G C T
SEQ. ID. NO. 42 T T T T G G G G C C A T G T T T G C A A A G A C C

SEQ. ID. NO. 44 G A C C A G A C C C T G G T C A T C A A G A C A T
SEQ. ID. NO. 42 T G G A G A G T C C A C G C C A T C T T C A A A A

SEQ. ID. NO. 44 T C C G C T T C C T G T C A C A G A A A C T C T T
SEQ. ID. NO. 42 A T G T G A A A A T G A A G A A G A A G A T C A T

SEQ. ID. NO. 44 T A T C T C C G T C T C A G T T C T C T C C A G C
SEQ. ID. NO. 42 C A A G G A C C A G A A A C T G C T T G T G A T C

SEQ. ID. NO. 44 C T G G G C A T T G T C C T A G C T G T T G T C T
SEQ. ID. NO. 42 G T G G G G G C A T G C T G C T G A T C G A C C

SEQ. ID. NO. 44 G T C T G T C C T T T A A C A T C T A C A A C T C
SEQ. ID. NO. 42 T G T G T A T C C T G A T C T G C T G G C A G G C

SEQ. ID. NO. 44 A C A T G T C C G T T A T A T C C A G A A C T C A
SEQ. ID. NO. 42 T G T G G A C C C C C T G C G A A G G A C A G T G

SEQ. ID. NO. 44 C A G C C C A A C C T G A A C A A C C T G A C T G
SEQ. ID. NO. 42 G A G A A G T A C A G C A T G G A G C C G G A C C

SEQ. ID. NO. 44 C T G T G G G C T G C T C A C T G G C T T T A G C
SEQ. ID. NO. 42 C A G C A G G A C G G G A T A T C T C C A T C C G

Figure 13f

SEQ. ID. NO. 44 T G C T G T C T T C C C C C T G G G G C T C G A T
SEQ. ID. NO. 42 C C C T C T C C T G G A G C A C T G T G A G A A C

SEQ. ID. NO. 44 G G T T A C C A C A T T G G G A G G A A C C A G T
SEQ. ID. NO. 42 A C C C A T A T G A C C A T C T G G C T T G G C A

SEQ. ID. NO. 44 T T C C T T T C G T C T G C C A G G C C C G C C T
SEQ. ID. NO. 42 T C G T C T A T G C C T A C A A G G G A C T T C T

SEQ. ID. NO. 44 C T G G C T C C T G G G C C T G G G C T T T A G T
SEQ. ID. NO. 42 C A T G T T G T T C G G T T G T T T C T T A G C T

SEQ. ID. NO. 44 C T G G G C T A C G G T T C C A T G T T C A C C A
SEQ. ID. NO. 42 T G G G A G A C C C G C A A C G T C A G C A T C C

SEQ. ID. NO. 44 A G A T T T G G T G G G T C C A C A C G G T C T T
SEQ. ID. NO. 42 C C G C A C T C A A C G A C A G C A A G T A C A T

SEQ. ID. NO. 44 C A C A A A G A A G G A A G A A A A G A A G G A G
SEQ. ID. NO. 42 C G G G A T G A G T G T C T A C A A C G T G G G G

SEQ. ID. NO. 44 T G G A G G A A G A C T C T G G A A C C C T G G A
SEQ. ID. NO. 42 A T C A T G T G C A T C A T C G G G G C C G C T G

SEQ. ID. NO. 44 A G C T G T A T G C C A C A G T G G G C C T G C T
SEQ. ID. NO. 42 T C T C C T T C C T G A C C C G G G A C C A G C C

SEQ. ID. NO. 44 G G T G G G C A T G G A T G T C C T C A C T C T C
SEQ. ID. NO. 42 C A A T G T G C A G T T C T G C A T C G T G G C T

SEQ. ID. NO. 44 G C C A T C T G G C A G A T C G T G G A C C C T C
SEQ. ID. NO. 42 C T G G T C A T C A T C T T C T G C A G C A C C A

SEQ. ID. NO. 44 T G C A C C G G A C C A T T G A G A C A T T T G C
SEQ. ID. NO. 42 T C A C C C T C T G C C T G G T A T T C G T G C C

SEQ. ID. NO. 44 C A A G G A G G A A C C T A A G G A A G A T A T T
SEQ. ID. NO. 42 G A A G C T C A T C A C C C T G A G A A C A A A C

Figure 13g

SEQ. ID. NO. 44 G A C G T C T C T A T T C T G C C C C A G C T G G
SEQ. ID. NO. 42 C C A G A T G C A G C A A C G C A G A A C A G G C

SEQ. ID. NO. 44 A G C A T T G C A G C T C C A G G A A G A T G A A
SEQ. ID. NO. 42 G A T T C C A G T T C A C T C A G A A T C A G A A

SEQ. ID. NO. 44 T A C A T G G C T T G G C A T T T T C T A T G G T
SEQ. ID. NO. 42 G A A A G A A G A T T C T A A A A C G T C C A C C

SEQ. ID. NO. 44 T A C A A G G G G C T G C T G C T G C T G C T G G
SEQ. ID. NO. 42 T C G G T C A C C A G T G T G A A C C A A G C C A

SEQ. ID. NO. 44 G A A T C T T C C T T G C T T A T G A G A C C A A
SEQ. ID. NO. 42 G C A C A T C C C G C C T G G A G G G C C T A C A

SEQ. ID. NO. 44 G A G T G T G T C C A C T G A G A A G A T C A A T
SEQ. ID. NO. 42 G T C A G A A A A C C A T C G C C T G C G A A T G

SEQ. ID. NO. 44 G A T C A C C G G G C T G T G G G C A T G G C T A
SEQ. ID. NO. 42 A A G A T C A C A G A G C T G G A T A A A G A C T

SEQ. ID. NO. 44 T C T A C A A T G T G G C A G T C C T G T G C C T
SEQ. ID. NO. 42 T G G A A G A G G T C A C C A T G C A G C T G C A

SEQ. ID. NO. 44 C A T C A C T G C T C C T G T C A C C A T G A T T
SEQ. ID. NO. 42 G G A C A C A C C A G A A A A G A C C A C C T A C

SEQ. ID. NO. 44 C T G T C C A G C C A G C A G G A T G C A G C C T
SEQ. ID. NO. 42 A T T A A A C A G A A C C A C T A C C A A G A G C

SEQ. ID. NO. 44 T T G C C T T T G C C T C T C T T G C C A T A G T
SEQ. ID. NO. 42 T C A A T G A C A T C C T C A A C C T G G G A A A

SEQ. ID. NO. 44 T T T C T C C T C C T A T A T C A C T C T T G T T
SEQ. ID. NO. 42 C T T C A C T G A G A G C A C A G A T G G A G G A

SEQ. ID. NO. 44 G T G C T C T T T G T G C C C A A G A T G C G C A
SEQ. ID. NO. 42 A A G G C C A T T T T A A A A A A T C A C C T C G

Figure 13h

SEQ. ID. NO. 44 G G C T G A T C A C C C G A G G G G A A T G G C A
SEQ. ID. NO. 42 A T C A A A A T C C C C A G C T A C A G T G G A A

SEQ. ID. NO. 44 G T C G G A G G C G C A G G A C A C C A T G A A G
SEQ. ID. NO. 42 C A C A A C A G A G C C C T C T C G A A C A T G C

SEQ. ID. NO. 44 A C A G G G T C A T C G A C C A A C A A C A A C G
SEQ. ID. NO. 42 A A A G A T C C T A T A G A A G A T A T A A A C T

SEQ. ID. NO. 44 A G G A G G A G A A G T C C C G G C T G T T G G A
SEQ. ID. NO. 42 C T C C A G A A C A C A T C C A G C G T C G G C T

SEQ. ID. NO. 44 G A A G G A G A A C C G T G A A C T G G A A A A G
SEQ. ID. NO. 42 G T C C C T C C A G C T C C C C A T C C T C C A C

SEQ. ID. NO. 44 A T C A T T G C T G A G A A A G A G G A G C G T G
SEQ. ID. NO. 42 C A C G C C T A C C T C C C A T C C A T C G G A G

SEQ. ID. NO. 44 T C T C T G A A C T G C G C C A T C A A C T C C A
SEQ. ID. NO. 42 G C G T G G A C G C C A G C T G T G T C A G C C C

SEQ. ID. NO. 44 G T C T C G G C A G C A G C T C C G C T C C C G G
SEQ. ID. NO. 42 C T G C G T C A G C C C C A C C G C C A G C C C C

SEQ. ID. NO. 44 C G C C A C C C A C C G A C A C C C C C A G A A C
SEQ. ID. NO. 42 C G C C A C A G A C A T G T G C C A C C C T C C T

SEQ. ID. NO. 44 C C T C T G G G G G C C T G C C C A G G G G A C C
SEQ. ID. NO. 42 T C C G A G T C A T G G T C T C G G G C C T G G C

SEQ. ID. NO. 44 C C C T G A G C C C C C C G A C C G G C T T A G C
SEQ. ID. NO. 42 G G C C G C C A T G A C T C T G G A G T C C A T C

SEQ. ID. NO. 44 T G T G A T G G G A G T C G A G T G C A T T T G C
SEQ. ID. NO. 42 A T G G C G T G C T G C C T G A G C G A G G A G G

SEQ. ID. NO. 44 T T T A T A A G G C G G C C G C C A T G A C T C T
SEQ. ID. NO. 42 C C A A G G A A G C C C G G C G G A T C A A C G A

Figure 13i

SEQ. ID. NO. 44 G G A G T C C A T C A T G G C G T G C T G C C T G
SEQ. ID. NO. 42 C G A G A T C G A G C G G C A G C T C C G C A G G

SEQ. ID. NO. 44 A G C G A G G A G G C C A A G G A A G C C C G G C
SEQ. ID. NO. 42 G A C A A G C G G G A C G C C C G C C G G G A G C

SEQ. ID. NO. 44 G G A T C A A C G A C G A G A T C G A G C G G C A
SEQ. ID. NO. 42 T C A A G C T G C T G C T G C T C G G G A C A G G

SEQ. ID. NO. 44 G C T C C G C A G G G A C A A G C G G G A C G C C
SEQ. ID. NO. 42 A G A G A G T G G C A A G A G T A C G T T T A T C

SEQ. ID. NO. 44 C G C C G G G A G C T C A A G C T G C T G C T G C
SEQ. ID. NO. 42 A A G C A G A T G A G A A T C A T C C A T G G G T

SEQ. ID. NO. 44 T C G G G A C A G G A G A G A G T G G C A A G A G
SEQ. ID. NO. 42 C A G G A T A C T C T G A T G A A G A T A A A A G

SEQ. ID. NO. 44 T A C G T T T A T C A A G C A G A T G A G A A T C
SEQ. ID. NO. 42 G G G C T T C A C C A A G C T G G T G T A T C A G

SEQ. ID. NO. 44 A T C C A T G G G T C A G G A T A C T C T G A T G
SEQ. ID. NO. 42 A A C A T C T T C A C G G C C A T G C A G G C C A

SEQ. ID. NO. 44 A A G A T A A A A G G G G C T T C A C C A A G C T
SEQ. ID. NO. 42 T G A T C A G A G C C A T G G A C A C A C T C A A

SEQ. ID. NO. 44 G G T G T A T C A G A A C A T C T T C A C G G C C
SEQ. ID. NO. 42 G A T C C C A T A C A A G T A T G A G C A C A A T

SEQ. ID. NO. 44 A T G C A G G C C A T G A T C A G A G C C A T G G
SEQ. ID. NO. 42 A A G G C T C A T G C A C A A T T A G T T C G A G

SEQ. ID. NO. 44 A C A C A C T C A A G A T C C C A T A C A A G T A
SEQ. ID. NO. 42 A A G T T G A T G T G G A G A A G G T G T C T G C

SEQ. ID. NO. 44 T G A G C A C A A T A A G G C T C A T G C A C A A
SEQ. ID. NO. 42 T T T T G A G A A T C C A T A T G T A G A T G C A

Figure 13j

SEQ. ID. NO. 44 T T A G T T C G A G A A G T T G A T G T G G A G A
SEQ. ID. NO. 42 A T A A A G A G T T T A T G G A A T G A T C C T G

SEQ. ID. NO. 44 A G G T G T C T G C T T T T G A G A A T C C A T A
SEQ. ID. NO. 42 G A A T C C A G G A A T G C T A T G A T A G A C G

SEQ. ID. NO. 44 T G T A G A T G C A A T A A A G A G T T T A T G G
SEQ. ID. NO. 42 A C G A G A A T A T C A A T T A T C T G A C T C T

SEQ. ID. NO. 44 A A T G A T C C T G G A A T C C A G G A A T G C T
SEQ. ID. NO. 42 A C C A A A T A C T A T C T T A A T G A C T T G G

SEQ. ID. NO. 44 A T G A T A G A C G A C G A G A A T A T C A A T T
SEQ. ID. NO. 42 A C C G C G T A G C T G A C C C T G C C T A C C T

SEQ. ID. NO. 44 A T C T G A C T C T A C C A A A T A C T A T C T T
SEQ. ID. NO. 42 G C C T A C G C A A C A A G A T G T G C T T A G A

SEQ. ID. NO. 44 A A T G A C T T G G A C C G C G T A G C T G A C C
SEQ. ID. NO. 42 G T T C G A G T C C C C A C C A C A G G G A T C A

SEQ. ID. NO. 44 C T G C C T A C C T G C C T A C G C A A C A A G A
SEQ. ID. NO. 42 T C G A A T A C C C C T T T G A C T T A C A A A G

SEQ. ID. NO. 44 T G T G C T T A G A G T T C G A G T C C C C A C C
SEQ. ID. NO. 42 T G T C A T T T T C A G A A T G G T C G A T G T A

SEQ. ID. NO. 44 A C A G G G A T C A T C G A A T A C C C C T T T G
SEQ. ID. NO. 42 G G G G G C C A A A G G T C A G A G A G A A G A A

SEQ. ID. NO. 44 A C T T A C A A A G T G T C A T T T T C A G A A T
SEQ. ID. NO. 42 A A T G G A T A C A C T G C T T T G A A A A T G T

SEQ. ID. NO. 44 G G T C G A T G T A G G G G G C C A A A G G T C A
SEQ. ID. NO. 42 C A C C T C T A T C A T G T T T C T A G T A G C G

SEQ. ID. NO. 44 G A G A G A A G A A A A T G G A T A C A C T G C T
SEQ. ID. NO. 42 C T T A G T G A A T A T G A T C A A G T T C T G G

Figure 13k

SEQ. ID. NO. 44 T T G A A A A T G T C A C C T C T A T C A T G T T
SEQ. ID. NO. 42 T G G A G T C A G A C A A T G A G A A C C G A A T

SEQ. ID. NO. 44 T C T A G T A G C G C T T A G T G A A T A T G A T
SEQ. ID. NO. 42 G G A G G A A A G C A A G G C T C T C T T T A G A

SEQ. ID. NO. 44 C A A G T T C T C G T G G A G T C A G A C A A T G
SEQ. ID. NO. 42 A C A A T T A T C A C A T A C C C C T G G T T C C

SEQ. ID. NO. 44 A G A A C C G A A T G G A G G A A A G C A A G G C
SEQ. ID. NO. 42 A G A A C T C C T C G G T T A T T C T G T T C T T

SEQ. ID. NO. 44 T C T C T T T A G A A C A A T T A T C A C A T A C
SEQ. ID. NO. 42 A A A C A A G A A A G A T C T T C T A G A G G A G

SEQ. ID. NO. 44 C C C T G G T T C C A G A A C T C C T C G G T T A
SEQ. ID. NO. 42 A A A A T C A T G T A T T C C C A T C T A G T C G

SEQ. ID. NO. 44 T T C T G T T C T T A A A C A A G A A A G A T C T
SEQ. ID. NO. 42 A C T A C T T C C C A G A A T A T G A T G G A C C

SEQ. ID. NO. 44 T C T A G A G G A G A A A A T C A T G T A T T C C
SEQ. ID. NO. 42 C C A G A G A G A T G C C C A G G C A G C C C G A

SEQ. ID. NO. 44 C A T C T A G T C G A C T A C T T C C C A G A A T
SEQ. ID. NO. 42 G A A T T C A T T C T G A A G A T G T T C G T G G

SEQ. ID. NO. 44 A T G A T G G A C C C C A G A G A G A T G C C C A
SEQ. ID. NO. 42 A C C T G A A C C C A G A C A G T G A C A A A A T

SEQ. ID. NO. 44 G G C A G C C C G A G A A T T C A T T C T G A A G
SEQ. ID. NO. 42 T A A C T A C T C C C A C T T C A C G T G C G C C

SEQ. ID. NO. 44 A T G T T C G T G G A C C T G A A C C C A G A C A
SEQ. ID. NO. 42 A C A G A C A C C G A G A A T A T C C G C T T T G

SEQ. ID. NO. 44 G T G A C A A A A T T A T C T A C T C C C A C T T
SEQ. ID. NO. 42 T C T T T G C T G C C G T C A A G G A C A C C A T

Figure 13L

SEQ. ID. NO. 44	C A C G T G C G C C A C A G A C A C C G A G A A T
SEQ. ID. NO. 42	C C T C C A G T T G A A C C T G A A G G G C T G C
SEQ. ID. NO. 44	A T C C G C T T T G T C T T T G C T G C C G T C A
SEQ. ID. NO. 42	G G T C T G T A C
SEQ. ID. NO. 44	A G G A C A C C A T C C T C C A G T T G A A C C T
SEQ. ID. NO. 42	
SEQ. ID. NO. 44	G A A G G G C T G C G G T C T G T A C
SEQ. ID. NO. 42	

Figure 13M

ClustalW Formatted Alignments

SEQ. ID. NO. 45 M L L L L L L A P L F L R P P G A G G A Q T P N A
SEQ. ID. NO. 43 M A S P R S S G Q P G P P P P P P P P A R L L L

SEQ. ID. NO. 45 T S E G C Q I I H P P W E G G I R Y R G L T R D Q
SEQ. ID. NO. 43 L L L L P L L L P L A P G A W G W A R G A P R P P

SEQ. ID. NO. 45 V K A I N F L P V D Y E I E Y V C R G E R E V V G
SEQ. ID. NO. 43 P S S P P L S I M G L M P L T K E V A K G S I G R

SEQ. ID. NO. 45 P K V R K C L A N G S W T D M D T P S R C V R I C
SEQ. ID. NO. 43 G V L P A V E L A I E Q I R N E S L L R P Y F L D

SEQ. ID. NO. 45 S K S Y L T L E N G K V F L T G G D L P A L D G A
SEQ. ID. NO. 43 L R L Y D T E C D N A K G L K A F Y D A I K Y G P

SEQ. ID. NO. 45 R V D F R C D P D F H L V G S S R S I C S Q G Q W
SEQ. ID. NO. 43 N H L M V F G G V C P S V T S I I A E S L Q G W N

SEQ. ID. NO. 45 S T P K P H C Q V N R T P H S E R R A V Y I G A L
SEQ. ID. NO. 43 L V Q L S F A A T T P V L A D K K K Y P Y F F R T

SEQ. ID. NO. 45 F P M S G G W P G G Q A C Q P A V E M A L E D V N
SEQ. ID. NO. 43 V P S D N A V N P A I L K L L K H Y Q W K R V G T

SEQ. ID. NO. 45 S R R D I L P D Y E L K L I H H D S K C D P G Q A
SEQ. ID. NO. 43 L T Q D V Q R F S E V R N D L T G V L Y G E D I E

SEQ. ID. NO. 45 T K Y L Y E L L Y N D P I K I I L M P G C S S V S
SEQ. ID. NO. 43 I S D T E S F S N D P C T S V K K L K G N D V R I

SEQ. ID. NO. 45 T L V A E A A R M W N L I V L S Y G S S S P A L S
SEQ. ID. NO. 43 I L G Q F D Q N M A A K V F C C A Y E E N M Y G S

SEQ. ID. NO. 45 N R Q R F P T F F R T H P S A T L H N P T R V K L
SEQ. ID. NO. 43 K Y Q W I I P G W Y E P S W W E Q V H T E A N S S

Figure 14a

SEQ. ID. NO. 45 F E K W G W K K I A T I Q Q T T E V F T S T L D D
SEQ. ID. NO. 43 R C L R K N L L A A M E G Y I G V D F E P L S S K

SEQ. ID. NO. 45 L E E R V K E A G I E I T F R Q S F F S D P A V P
SEQ. ID. NO. 43 Q I K T I S G K T P Q Q Y E R E Y N N K R S G V G

SEQ. ID. NO. 45 V K N L K R Q D A R I I V G L F Y E T E A R K V F
SEQ. ID. NO. 43 P S K F H G Y A Y D G I W V I A K T L Q R A M E T

SEQ. ID. NO. 45 C E V Y K E R L F G K K Y V W F L I G W Y A D N W
SEQ. ID. NO. 43 L H A S S R H Q R I Q D F N Y T D H T L G R I I L

SEQ. ID. NO. 45 F K I Y D P S I N C T V D E M T E A V E G H I T T
SEQ. ID. NO. 43 N A M N E T N P F G V T G Q V V F R N G E R M G T

SEQ. ID. NO. 45 E I V M L N P A N T R S I S N M T S Q E F V E K L
SEQ. ID. NO. 43 I K F T Q F Q D S R E V K V G E Y N A V A D T L E

SEQ. ID. NO. 45 T K R L K R H P E E T G G - F Q E A P L A Y D A I
SEQ. ID. NO. 43 I I N D T I R F Q G S E P P K D K T I I L E Q L R

SEQ. ID. NO. 45 W A L A L A L N K T S G G G G R S G V R L E D F N
SEQ. ID. NO. 43 K I S L P L Y S I L S A L T I L G M I M A S A F L

SEQ. ID. NO. 45 Y N N Q T I T D Q I Y R A M N S S S F E G V S G H
SEQ. ID. NO. 43 F F N I K N R N Q K L I K M S S P Y M N N L I I L

SEQ. ID. NO. 45 V V F D A S G S R M A W T L I E Q L Q G G S Y K K
SEQ. ID. NO. 43 G G M L S Y A S I F L F G L D G S F V S E K T F E

SEQ. ID. NO. 45 I G Y Y D S T K D D L S W S K T D K W I G G S P P
SEQ. ID. NO. 43 T L C T V R T W I L T V G Y T T A F G A M F A K T

SEQ. ID. NO. 45 A D Q T L V I K T F R F L S Q K L F I S V S V L S
SEQ. ID. NO. 43 W R V H A I F K N V K M K K K I I K D Q K L L V I

SEQ. ID. NO. 45 S L G I V L A V V C L S F N I Y N S H V R Y I Q N
SEQ. ID. NO. 43 V G G M L L I D L C I L I C W Q A V D P L R R T V

Figure 14b

SEQ. ID. NO. 45 S Q P N L N N L T A V G C S L A L A A V F P L G L
SEQ. ID. NO. 43 E K Y S M E P D P A G R D I S I R P L L E H C E N

SEQ. ID. NO. 45 D G Y H I G R N Q F P F V C Q A R L W L L G L G F
SEQ. ID. NO. 43 T H M T I W L G I V Y A Y K G L L M L F G C F L A

SEQ. ID. NO. 45 S L G Y G S M F T K I W W V H T V F T K K E E K K
SEQ. ID. NO. 43 W E T R N V S I P A L N D S K Y I G M S V Y N V G

SEQ. ID. NO. 45 E W R K T L E P W K L Y A T V G L L V G M D V L T
SEQ. ID. NO. 43 I M C I I G A A V S F L T R D Q P N V Q F C I V A

SEQ. ID. NO. 45 L A I W Q I V D P L H R T I E T F A K E E P K E D
SEQ. ID. NO. 43 L V I I F C S T I T L C L V F V P K L I T L R T N

SEQ. ID. NO. 45 I D V S I L P Q L E H C S S R K M N T W L G I F Y
SEQ. ID. NO. 43 P D A A T Q N R R F Q F T Q N Q K K E D S K T S T

SEQ. ID. NO. 45 G Y K G L L L L L G I F L A Y E T K S V S T E K I
SEQ. ID. NO. 43 S V T S V N Q A S T S R L E G L Q S E N H R L R M

SEQ. ID. NO. 45 N D H R A V G M A I Y N V A V L C L I T A P V T M
SEQ. ID. NO. 43 K I T E L D K D L E E V T M Q L Q D T P E K T T Y

SEQ. ID. NO. 45 I L S S Q Q D A A F A F A S L A I V F S S Y I T L
SEQ. ID. NO. 43 I K Q N H Y Q E L N D I L N L G N F T E S T D G G

SEQ. ID. NO. 45 V V L F V P K M R R L I T R G E W Q S E A Q D T M
SEQ. ID. NO. 43 K A I L K N H L D Q N P Q L Q W N T T E P S R T C

SEQ. ID. NO. 45 K T G S S T N N N E E E K S R L L E K E N R E L E
SEQ. ID. NO. 43 K D P I E D I N S P E H I Q R R L S L Q L P I L H

SEQ. ID. NO. 45 K I I A E K E E R V S E L R H Q L Q S R Q Q L R S
SEQ. ID. NO. 43 H A Y L P S I G G V D A S C V S P C V S P T A S P

SEQ. ID. NO. 45 R R H P P T P P E P S G G L P R G P P E P P D R L
SEQ. ID. NO. 43 R H R H V P P S F R V M V S G L A A A M T L E S I

Figure 14c

SEQ. ID. NO. 45 S C D G S R V H L L Y K A A A M T L E S I M A C C
SEQ. ID. NO. 43 M A C C L S E E A K E A R R I N D E I E R Q L R R

SEQ. ID. NO. 45 L S E E A K E A R R I N D E I E R Q L R R D K R D
SEQ. ID. NO. 43 D K R D A R R E L K L L L L G T G E S G K S T F I

SEQ. ID. NO. 45 A R R E L K L L L L G T G E S G K S T F I K Q M R
SEQ. ID. NO. 43 K Q M R I I H G S G Y S D E D K R G F T K L V Y Q

SEQ. ID. NO. 45 I I H G S G Y S D E D K R G F T K L V Y Q N I F T
SEQ. ID. NO. 43 N I F T A M Q A M I R A M D T L K I P Y K Y E H N

SEQ. ID. NO. 45 A M Q A M I R A M D T L K I P Y K Y E H N K A H A
SEQ. ID. NO. 43 K A H A Q L V R E V D V E K V S A F E N P Y V D A

SEQ. ID. NO. 45 Q L V R E V D V E K V S A F E N P Y V D A I K S L
SEQ. ID. NO. 43 I K S L W N D P G I Q E C Y D R R R E Y Q L S D S

SEQ. ID. NO. 45 W N D P G I Q E C Y D R R R E Y Q L S D S T K Y Y
SEQ. ID. NO. 43 T K Y Y L N D L D R V A D P A Y L P T Q Q D V L R

SEQ. ID. NO. 45 L N D L D R V A D P A Y L P T Q Q D V L R V R V P
SEQ. ID. NO. 43 V R V P T T G I I E Y P F D L Q S V I F R M V D V

SEQ. ID. NO. 45 T T G I I E Y P F D L Q S V I F R M V D V G G Q R
SEQ. ID. NO. 43 G G Q R S E R R K W I H C F E N V T S I M F L V A

SEQ. ID. NO. 45 S E R R K W I H C F E N V T S I M F L V A L S E Y
SEQ. ID. NO. 43 L S E Y D Q V L V E S D N E N R M E E S K A L F R

SEQ. ID. NO. 45 D Q V L V E S D N E N R M E E S K A L F R T I I T
SEQ. ID. NO. 43 T I I T Y P W F Q N S S V I L F L N K K D L L E E

SEQ. ID. NO. 45 Y P W F Q N S S V I L F L N K K D L L E E K I M Y
SEQ. ID. NO. 43 K I M Y S H L V D Y F P E Y D G P Q R D A Q A A R

SEQ. ID. NO. 45 S H L V D Y F P E Y D G P Q R D A Q A A R E F I L
SEQ. ID. NO. 43 E F I L K M F V D L N P D S D K I N Y S H F T C A

Figure 14d

SEQ. ID. NO. 45	K M F V D L N P D S D K I I Y S H F T C A T D T E
SEQ. ID. NO. 43	T D T E N I R F V F A A V K D T I L Q L N L K G C

SEQ. ID. NO. 45	N I R F V F A A V K D T I L Q L N L K G C G L Y
SEQ. ID. NO. 43	G L Y

Figure 14e

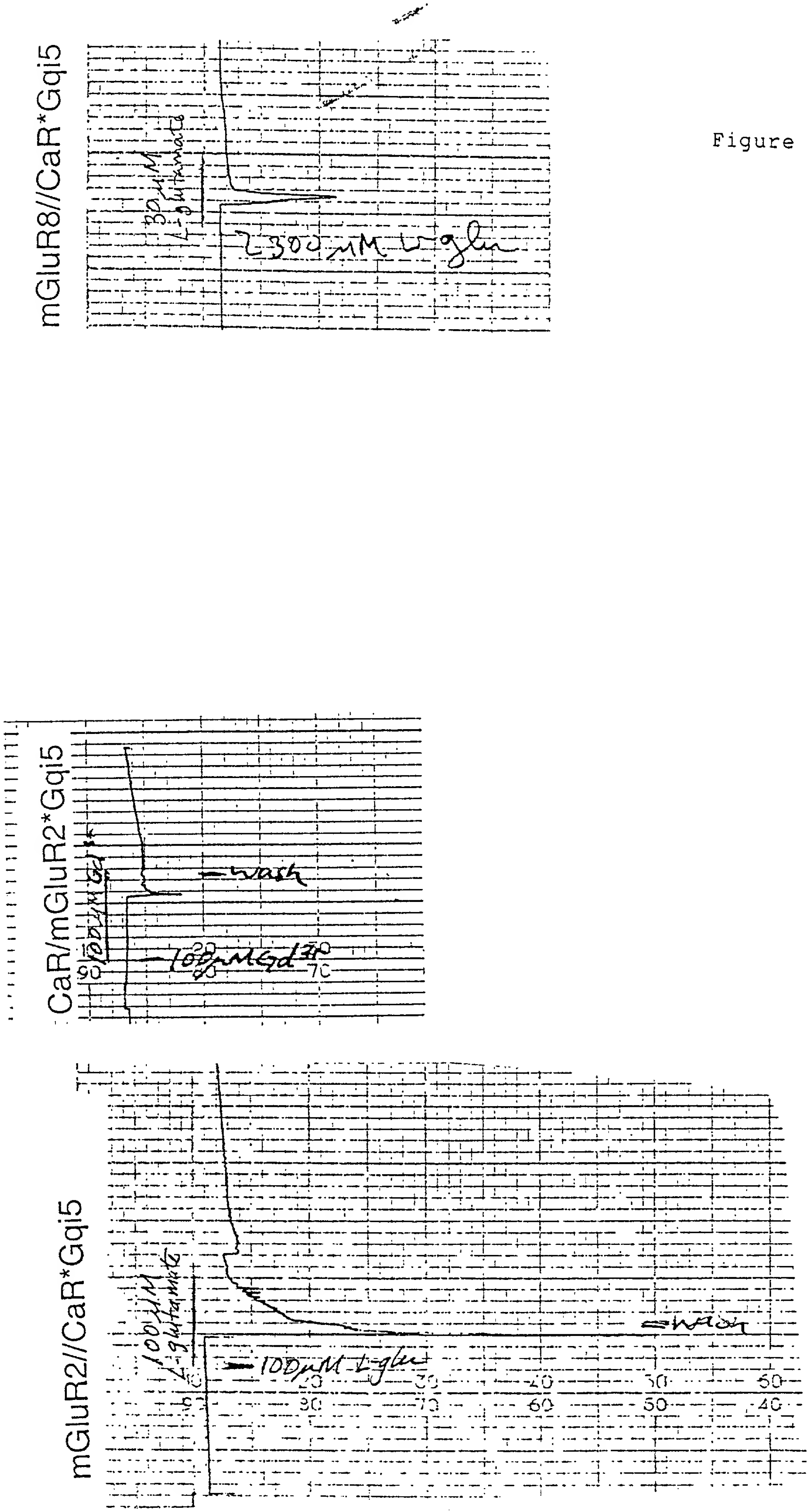

mGluR8//CaR*Gqi5
30 μM L-glutamate
2300 μM L-glu
CaR/mGluR2*Gqi5
100 μM Gd3+
wash
mGluR2//CaR*Gqi5
100 μM L-glutamate
100 μM L-glu
wash

Figure 15

FIGURE 16A

SEQ. ID. NO. 48 M V C E G K R S A S C P C F F L L T A K F Y W I L T M M Q R
SEQ. ID. NO. 49 M V C E G K R S A S C P C F F L L T A K F Y W I L T M M Q R
SEQ. ID. NO. 50 M V C E G K R S A S C P C F F L L T A K F Y W I L T M M Q R

SEQ. ID. NO. 48 T H S Q E Y A H S I R I D G D I T L G G L F P V H G R G S E
SEQ. ID. NO. 49 T H S Q E Y A H S I R I D G D I T L G G L F P V H G R G S E
SEQ. ID. NO. 50 T H S Q E Y A H S I R V D G D I I L G G L F P V H A K G E R

SEQ. ID. NO. 48 G K P C G E L K K E K G I H R L E A M L F A L D R I N N D P
SEQ. ID. NO. 49 G K P C G E L K K E K G I H R L E A M L F A L D R I N N D P
SEQ. ID. NO. 50 G V P C G E L K K E K G I H R L E A M L Y A I D Q I N K D P

SEQ. ID. NO. 48 D L L P N I T L G A R I L D T C S R D T H A L E Q S L T F V
SEQ. ID. NO. 49 D L L P N I T L G A R I L D T C S R D T H A L E Q S L T F V
SEQ. ID. NO. 50 D L L S N I T L G V R I L D T C S R D T Y A L E Q S L T F V

SEQ. ID. NO. 48 Q A L I E K D G T E V R C G S G G P P I I T K P E R V V G V
SEQ. ID. NO. 49 Q A L I E K D G T E V R C G S G G P P I I T K P E R V V G V
SEQ. ID. NO. 50 Q A L I E K D A S D V K C A N G D P P I F T K P D K I S G V

SEQ. ID. NO. 48 I G A S G S S V S I M V A N I L R L F K I P Q I S Y A S T A
SEQ. ID. NO. 49 I G A S G S S V S I M V A N I L R L F K I P Q I S Y A S T A
SEQ. ID. NO. 50 I G A A A S S V S I M V A N I L R L F K I P Q I S Y A S T A

SEQ. ID. NO. 48 P D L S D N S R Y D F F S R V V P S D T Y Q A Q A M V D I V
SEQ. ID. NO. 49 P D L S D N S R Y D F F S R V V P S D T Y Q A Q A M V D I V
SEQ. ID. NO. 50 P E L S D N T R Y D F F S R V V P P D S Y Q A Q A M V D I V

SEQ. ID. NO. 48 R A L K W N Y V S T V A S E G S Y G E S G V E A F I Q K S R
SEQ. ID. NO. 49 R A L K W N Y V S T V A S E G S Y G E S G V E A F I Q K S R
SEQ. ID. NO. 50 T A L G W N Y V S T L A S E G N Y G E S G V E A F T Q I S R

SEQ. ID. NO. 48 E D G G V C I A Q S V K I P R E P K A G E F D K I I R R L L
SEQ. ID. NO. 49 E D G G V C I A Q S V K I P R E P K A G E F D K I I R R L L
SEQ. ID. NO. 50 E I G G V C I A Q S Q K I P R E P R P G E F E K I I K R L L

FIGURE 16B

SEQ. ID. NO. 48 E T S N A R A V I I F A N E D D I R R V L E A A R R A N Q T
SEQ. ID. NO. 49 E T S N A R A V I I F A N E D D I R R V L E A A R R A N Q T
SEQ. ID. NO. 50 E T P N A R A V I M F A N E D D I R R I L E A A K K L N Q S

SEQ. ID. NO. 48 G H F F W M G S D S W G S K I A P V L H L E E V A E G A V T
SEQ. ID. NO. 49 G H F F W M G S D S W G S K I A P V L H L E E V A E G A V T
SEQ. ID. NO. 50 G H F L W I G S D S W G S K I A P V Y Q Q E E I A E G A V T

SEQ. ID. NO. 48 I L P K R M S V R G F D R Y F S S R T L D N N R R N I W F A
SEQ. ID. NO. 49 I L P K R M S V R G F D R Y F S S R T L D N N R R N I W F A
SEQ. ID. NO. 50 I L P K R A S I D G F D R Y F R S R T L A N N R R N V W F A

SEQ. ID. NO. 48 E F W E D N F H C K L S R H A L K K G S H V K K C T N R E R
SEQ. ID. NO. 49 E F W E D N F H C K L S R H A L K K G S H V K K C T N R E R
SEQ. ID. NO. 50 E F W E E N F G C K L G S H G K R N - S H I K K C T G L E R

SEQ. ID. NO. 48 I G Q D S A Y E Q E G K V Q F V I D A V Y A M G H A L H A M
SEQ. ID. NO. 49 I G Q D S A Y E Q E G K V Q F V I D A V Y A M G H A L H A M
SEQ. ID. NO. 50 I A R D S S Y E Q E G K V Q F V I D A V Y S M A Y A L H N M

SEQ. ID. NO. 48 H R D L C P G R V G L C P R M D P V D G T Q L L K Y I R N V
SEQ. ID. NO. 49 H R D L C P G R V G L C P R M D P V D G T Q L L K Y I R N V
SEQ. ID. NO. 50 H K D L C P G Y I G L C P R M S T I D G K E L L G Y I R A V

SEQ. ID. NO. 48 N F S G I A G N P V T F N E N G D A P G R Y D I Y Q Y Q L R
SEQ. ID. NO. 49 N F S G I A G N P V T F N E N G D A P G R Y D I Y Q Y Q L R
SEQ. ID. NO. 50 N F N G S A G T P V T F N E N G D A P G R Y D I F Q Y Q I T

SEQ. ID. NO. 48 N D S A E Y K V I G S W T D H L H L R I E R M H W P G S G Q
SEQ. ID. NO. 49 N D S A E Y K V I G S W T D H L H L R I E R M H W P G S G Q
SEQ. ID. NO. 50 N K S T E Y K V I G H W T N Q L H L K V E D M Q W A H R E H

SEQ. ID. NO. 48 Q L P R S I C S L P C Q P G E R K K T V K G M P C C W H C E
SEQ. ID. NO. 49 Q L P R S I C S L P C Q P G E R K K T V K G M P C C W H C E
SEQ. ID. NO. 50 T H P A S V C S L P C K P G E R K K T V K G V P C C W H C E

SEQ. ID. NO. 48 P C T G Y Q Y Q V D R Y T C K T C P Y D M R P T E N R T G C
SEQ. ID. NO. 49 P C T G Y Q Y Q V D R Y T C K T C P Y D M R P T E N R T G C
SEQ. ID. NO. 50 R C E G Y N Y Q V D E L S C E L C P L D Q R P N M N R T G C

FIGURE 16C

SEQ. ID. NO. 48 R P I P I I K L E W G S P W A V L P L F L A V V G I A A T L
SEQ. ID. NO. 49 R P I P I I K L E W G S P W A V L P L F L A V V G I A A T L
SEQ. ID. NO. 50 Q L I P I I K L E W H S P W A V V P V F V A I L G I I A T T

SEQ. ID. NO. 48 F V V I T F V R Y N D T P I V K A S G R E L S Y V L L A G I
SEQ. ID. NO. 49 F V V I T F V R Y N D T P I V K A S G R E L S Y V L L A G I
SEQ. ID. NO. 50 F V I V T F V R Y N D T P I V R A S G R E L S Y V L L T G I

SEQ. ID. NO. 48 F L C Y A T T F L M I A E P D L G T C S L R R I F L G L G M
SEQ. ID. NO. 49 F L C Y A T T F L M I A E P D L G T C S L R R I F L G L G M
SEQ. ID. NO. 50 F L C Y S I T F L M I A A P D T I I C S F R R V F L G L G M

SEQ. ID. NO. 48 S I S Y A A L L T K T N R I Y R I F E Q G K R S V S A P R F
SEQ. ID. NO. 49 S I S Y A A L L T K T N R I Y R I F E Q G K R S V S A P R F
SEQ. ID. NO. 50 C F S Y A A L L T K T N R I H R I F E Q G K K S V T A P K F

SEQ. ID. NO. 48 I S P A S Q L A I T F S L I S L Q L L G I C V W F V V D P S
SEQ. ID. NO. 49 I S P A S Q L A I T F S L I S L Q L L G I C V W F V V D P S
SEQ. ID. NO. 50 I S P A S Q L V I T F S L I S V Q L L G V F V W F V V D P P

SEQ. ID. NO. 48 H S V V D F Q D Q R T L D P R F A R G V L K C D I S D L S L
SEQ. ID. NO. 49 H S V V D F Q D Q R T L D P R F A R G V L K C D I S D L S L
SEQ. ID. NO. 50 H I I I D Y G E Q R T L D P E K A R G V L K C D I S D L S L

SEQ. ID. NO. 48 I C L L G Y S M L L M V T C T V Y A I K T R G V P E T F N E
SEQ. ID. NO. 49 I C L L G Y S M L L M V T C T V Y A I K T R G V P E T F N E
SEQ. ID. NO. 50 I C S L G Y S I L L M V T C T V Y A I K T R G V P E T F N E

SEQ. ID. NO. 48 A K P I G F T M Y T T C I V W L A F I P I F F G T S Q S A D
SEQ. ID. NO. 49 A K P I G F T M Y T T C I V W L A F I P I F F G T S Q S A D
SEQ. ID. NO. 50 A K P I G F T M Y T T C I I W L A F I P I F F G T A Q S A E

SEQ. ID. NO. 48 K L Y I Q T T T L T V S V S L S A S V S L G M L Y M P K V Y
SEQ. ID. NO. 49 K L Y I Q T T T L T V S V S L S A S V S L G M L Y M P K V Y
SEQ. ID. NO. 50 K M Y I Q T T T L T V S M S L S A S V S L G M L Y M P K V Y

SEQ. ID. NO. 48 I I L F H P E Q N V P K R K R S L K A V V T A A T M S N K F
SEQ. ID. NO. 49 I I L F H P E Q N T I E E V R C S T A A H A F K V A A R A T
SEQ. ID. NO. 50 I I I F H P E Q N T I E E V R C S T A A H A F K V A A R A T

FIGURE 16D

SEQ. ID. NO. 48 T Q K G N F R P N G E A K S E L C E N L E A P A L A T K Q T
SEQ. ID. NO. 49 L R R S N V S R K R S S S L G G S T G S T P S S S I S S K S
SEQ. ID. NO. 50 L R R S N V S R K R S S S L G G S T G S T P S S S I S S K S

SEQ. ID. NO. 48 Y V T Y T N H A I
SEQ. ID. NO. 49 N S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q Q Q Q P L
SEQ. ID. NO. 50 N S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q Q Q Q P L

SEQ. ID. NO. 48
SEQ. ID. NO. 49 T L P Q Q Q R S Q Q Q P R C K Q K V I F G S G T V T F S L S
SEQ. ID. NO. 50 T L P Q Q Q R S Q Q Q P R C K Q K V I F G S G T V T F S L S

SEQ. ID. NO. 48
SEQ. ID. NO. 49 F D E P Q K N A M A H G N S T H Q N S L E A Q K S S D T L T
SEQ. ID. NO. 50 F D E P Q K N A M A H G N S T H Q N S L E A Q K S S D T L T

SEQ. ID. NO. 48
SEQ. ID. NO. 49 R H Q P L L P L Q C G E T D L D L T V Q E T G L Q G P V G G
SEQ. ID. NO. 50 R H Q P L L P L Q C G E T D L D L T V Q E T G L Q G P V G G

SEQ. ID. NO. 48
SEQ. ID. NO. 49 D Q R P E V E D P E E L S P A L V V S S S Q S F V I S G G G
SEQ. ID. NO. 50 D Q R P E V E D P E E L S P A L V V S S S Q S F V I S G G G

SEQ. ID. NO. 48
SEQ. ID. NO. 49 S T V T E N V V N S A A A M T L E S I M A C C L S E E A K E
SEQ. ID. NO. 50 S T V T E N V V N S A A A M T L E S I M A C C L S E E A K E

SEQ. ID. NO. 48
SEQ. ID. NO. 49 A R R I N D E I E R Q L R R D K R D A R R E L K L L L L G T
SEQ. ID. NO. 50 A R R I N D E I E R Q L R R D K R D A R R E L K L L L L G T

SEQ. ID. NO. 48
SEQ. ID. NO. 49 G E S G K S T F I K Q M R I I H G S G Y S D E D K R G F T K
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SEQ. ID. NO. 50 L V Y Q N I F T A M Q A M I R A M D T L K I P Y K Y E H N K

FIGURE 16E

SEQ. ID. NO. 48
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SEQ. ID. NO. 50 A H A Q L V R E V D V E K V S A F E N P Y Y V D A I K S L W N

SEQ. ID. NO. 48
SEQ. ID. NO. 49 D P G I Q E C Y D R R R E Y Q L S D S T K Y Y L N D L D R V
SEQ. ID. NO. 50 D P G I Q E C Y D R R R E Y Q L S D S T K Y Y L N D L D R V

SEQ. ID. NO. 48
SEQ. ID. NO. 49 A D P A Y L P T Q Q D V L R V R V P T T G I I E Y P F D L Q
SEQ. ID. NO. 50 A D P A Y L P T Q Q D V L R V R V P T T G I I E Y P F D L Q

SEQ. ID. NO. 48
SEQ. ID. NO. 49 S V I F R M V D V G G Q R S E R R K W I H C F E N V T S I M
SEQ. ID. NO. 50 S V I F R M V D V G G Q R S E R R K W I H C F E N V T S I M

SEQ. ID. NO. 48
SEQ. ID. NO. 49 F L V A L S E Y D Q V L V E S D N E N R M E E S K A L F R T
SEQ. ID. NO. 50 F L V A L S E Y D Q V L V E S D N E N R M E E S K A L F R T

SEQ. ID. NO. 48
SEQ. ID. NO. 49 I I T Y P W F Q N S S V I L F L N K K D L L E E K I M Y S H
SEQ. ID. NO. 50 I I T Y P W F Q N S S V I L F L N K K D L L E E K I M Y S H

SEQ. ID. NO. 48
SEQ. ID. NO. 49 L V D Y F P E Y D G P Q R D A Q A A R E F I L K M F V D L N
SEQ. ID. NO. 50 L V D Y F P E Y D G P Q R D A Q A A R E F I L K M F V D L N

SEQ. ID. NO. 48
SEQ. ID. NO. 49 P D S D K I I Y S H F T C A T D T E N I R F V F A A V K D T
SEQ. ID. NO. 50 P D S D K I I Y S H F T C A T D T E N I R F V F A A V K D T

SEQ. ID. NO. 48
SEQ. ID. NO. 49 I L Q L N L K D C G L F
SEQ. ID. NO. 50 I L Q L N L K D C G L F

SEQUENCE LISTING

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GABAB RECEPTORS

<130> 241/086-CIP

<140> TO BE ASSIGNED
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<151> 1998-04-03

<150> PCT/US99/07333
<151> 1999-04-02

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Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Ala Lys Asp
        35                  40                  45

Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys Ile Arg Tyr Asn
    50                  55                  60

Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe Ala Ile Glu Glu
65                  70                  75                  80

Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Leu Thr Leu Gly Tyr Arg
                85                  90                  95

Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu Glu Ala Thr Leu
            100                 105                 110
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Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn Leu Asp Glu Phe
        115                 120                 125

Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala Val Val Gly Ala
    130                 135                 140

Thr Gly Ser Gly Val Ser Thr Ala Val Ala Asn Leu Leu Gly Leu Phe
145                 150                 155                 160

Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg Leu Leu Ser Asn
                165                 170                 175

Lys Asn Gln Phe Lys Ser Phe Leu Arg Thr Ile Pro Asn Asp Glu His
            180                 185                 190

Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe Arg Trp Asn Trp
        195                 200                 205

Val Gly Thr Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly Ile Glu
    210                 215                 220

Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys Ile Asp Phe Ser
225                 230                 235                 240

Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Glu Ile Gln His Val Val
                245                 250                 255

Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val Val Phe Ser Ser
            260                 265                 270

Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val Arg Arg Asn Ile
        275                 280                 285

Thr Gly Lys Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser Ser Leu
    290                 295                 300

Ile Ala Met Pro Gln Tyr Phe His Val Val Gly Gly Thr Ile Gly Phe
305                 310                 315                 320

Ala Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu Phe Leu Lys Lys
                325                 330                 335

Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala Lys Glu Phe Trp
            340                 345                 350

Glu Glu Thr Phe Asn Cys His Leu Gln Glu Gly Ala Lys Gly Pro Leu
        355                 360                 365

Pro Val Asp Thr Phe Leu Arg Gly His Glu Glu Ser Gly Asp Arg Phe
    370                 375                 380

Ser Asn Ser Ser Thr Ala Phe Arg Pro Leu Cys Thr Gly Asp Glu Asn
385                 390                 395                 400

Ile Ser Ser Val Glu Thr Pro Tyr Ile Asp Tyr Thr His Leu Arg Ile
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405 410 415

Ser Tyr Asn Val Tyr Leu Ala Val Tyr Ser Ile Ala His Ala Leu Gln
420 425 430

Asp Ile Tyr Thr Cys Leu Pro Gly Arg Gly Leu Phe Thr Asn Gly Ser
435 440 445

Cys Ala Asp Ile Lys Lys Val Glu Ala Trp Gln Val Leu Lys His Leu
450 455 460

Arg His Leu Asn Phe Thr Asn Asn Met Gly Glu Gln Val Thr Phe Asp
465 470 475 480

Glu Cys Gly Asp Leu Val Gly Asn Tyr Ser Ile Ile Asn Trp His Leu
485 490 495

Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val Gly Tyr Tyr Asn
500 505 510

Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn Glu Glu Lys Ile
515 520 525

Leu Trp Ser Gly Phe Ser Arg Glu Val Pro Phe Ser Asn Cys Ser Arg
530 535 540

Asp Cys Leu Ala Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr
545 550 555 560

Cys Cys Phe Glu Cys Val Glu Cys Pro Asp Gly Glu Tyr Ser Asp Glu
565 570 575

Thr Asp Ala Ser Ala Cys Asn Lys Cys Pro Asp Asp Phe Trp Ser Asn
580 585 590

Glu Asn His Thr Ser Cys Ile Ala Lys Glu Ile Glu Phe Leu Ser Trp
595 600 605

Thr Glu Pro Phe
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Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
20 25 30

Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
        35   40   45

Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
    50   55   60

Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
65   70   75   80

Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
                85   90   95

Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val
            100   105   110

Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp
        115   120   125

Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Ile
    130   135   140

Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn
145   150   155   160

Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe
                165   170   175

Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val
            180   185   190

Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp
        195   200   205

Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln
    210   215   220

Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile
225   230   235   240

Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala
                245   250   255

Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro
            260   265   270

Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro
        275   280   285

Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp
    290   295   300

Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr
305   310   315   320

Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu
                325   330   335

Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys
340 345 350

Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu
355 360 365

Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe
370 375 380

Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp
385 390 395 400

Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr
405 410 415

Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro
420 425 430

Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu
435 440 445

Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe
450 455 460

Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala
465 470 475 480

Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu
485 490 495

Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala
500 505 510

Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp
515 520 525

Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly
530 535 540

Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu
545 550 555 560

Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp
565 570 575

Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys
580 585 590

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Met Gly Pro Gly Ala Pro Phe Ala Arg Val Gly Trp Pro Leu Pro Leu
1   5   10   15

Leu Val Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser
            20   25   30

Pro His Leu Pro Arg Pro His Ser Arg Val Pro Pro His Pro Ser Ser
        35   40   45

Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly
    50   55   60

Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu
65   70   75   80

Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu
                85   90   95

Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu
            100   105   110

Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly
        115   120   125

Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn
    130   135   140

Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg
145   150   155   160

Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His
                165   170   175

Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile
            180   185   190

Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp
        195   200   205

Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln
    210   215   220

Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln
225   230   235   240

Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys
                245   250   255

Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val
            260   265   270

Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp
275 280 285

Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala Val Glu Gly
290 295 300

His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser
305 310 315 320

Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg
325 330 335

Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu
340 345 350

Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser
355 360 365

Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn
370 375 380

Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser
385 390 395 400

Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg
405 410 415

Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys
420 425 430

Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr
435 440 445

Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln Thr Leu Val Ile
450 455 460

Lys Thr Phe Arg Phe Leu Ser Gln Lys
465 470

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Leu Pro Leu Ala Pro Gly Ala Trp Gly Trp Ala Arg Gly Ala Pro Arg

35 40 45

Pro Pro Pro Ser Ser Pro Pro Leu Ser Ile Met Gly Leu Met Pro Leu
50 55 60

Thr Lys Glu Val Ala Lys Gly Ser Ile Gly Arg Gly Val Leu Pro Ala
65 70 75 80

Val Glu Leu Ala Ile Glu Gln Ile Arg Asn Glu Ser Leu Leu Arg Pro
85 90 95

Tyr Phe Leu Asp Leu Arg Leu Tyr Asp Thr Glu Cys Asp Asn Ala Lys
100 105 110

Gly Leu Lys Ala Phe Tyr Asp Ala Ile Lys Tyr Gly Pro Asn His Leu
115 120 125

Met Val Phe Gly Gly Val Cys Pro Ser Val Thr Ser Ile Ile Ala Glu
130 135 140

Ser Leu Gln Gly Trp Asn Leu Val Gln Leu Ser Phe Ala Ala Thr Thr
145 150 155 160

Pro Val Leu Ala Asp Lys Lys Lys Tyr Pro Tyr Phe Phe Arg Thr Val
165 170 175

Pro Ser Asp Asn Ala Val Asn Pro Ala Ile Leu Lys Leu Leu Lys His
180 185 190

Tyr Gln Trp Lys Arg Val Gly Thr Leu Thr Gln Asp Val Gln Arg Phe
195 200 205

Ser Glu Val Arg Asn Asp Leu Thr Gly Val Leu Tyr Gly Glu Asp Ile
210 215 220

Glu Ile Ser Asp Thr Glu Ser Phe Ser Asn Asp Pro Cys Thr Ser Val
225 230 235 240

Lys Lys Leu Lys Gly Asn Asp Val Arg Ile Ile Leu Gly Gln Phe Asp
245 250 255

Gln Asn Met Ala Ala Lys Val Phe Cys Cys Ala Tyr Glu Glu Asn Met
260 265 270

Tyr Gly Ser Lys Tyr Gln Trp Ile Ile Pro Gly Trp Tyr Glu Pro Ser
275 280 285

Trp Trp Glu Gln Val His Thr Glu Ala Asn Ser Ser Arg Cys Leu Arg
290 295 300

Lys Asn Leu Leu Ala Ala Met Glu Gly Tyr Ile Gly Val Asp Phe Glu
305 310 315 320

Pro Leu Ser Ser Lys Gln Ile Lys Thr Ile Ser Gly Lys Thr Pro Gln
325 330 335

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Gln Tyr Glu Arg Glu Tyr Asn Asn Lys Arg Ser Gly Val Gly Pro Ser
            340                 345                 350

Lys Phe His Gly Tyr Ala Tyr Asp Gly Ile Trp Val Ile Ala Lys Thr
        355                 360                 365

Leu Gln Arg Ala Met Glu Thr Leu His Ala Ser Ser Arg His Gln Arg
    370                 375                 380

Ile Gln Asp Phe Asn Tyr Thr Asp His Thr Leu Gly Arg Ile Ile Leu
385                 390                 395                 400

Asn Ala Met Asn Glu Thr Asn Phe Phe Gly Val Thr Gly Gln Val Val
                405                 410                 415

Phe Arg Asn Gly Glu Arg Met Gly Thr Ile Lys Phe Thr Gln Phe Gln
            420                 425                 430

Asp Ser Arg Glu Val Lys Val Gly Glu Tyr Asn Ala Val Ala Asp Thr
        435                 440                 445

Leu Glu Ile Ile Asn Asp Thr Ile Arg Phe Gln Gly Ser Glu Pro Pro
    450                 455                 460

Lys Asp Lys Thr Ile Ile Leu Glu Gln Leu Arg Lys Ile Ser Leu Pro
465                 470                 475                 480


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Leu Thr Ala Lys Phe Tyr Trp Ile Leu Thr Met Met Gln Arg Thr His
            20                  25                  30

Ser Gln Glu Tyr Ala His Ser Ile Arg Val Asp Gly Asp Ile Ile Leu
        35                  40                  45

Gly Gly Leu Phe Pro Val His Ala Lys Gly Glu Arg Gly Val Pro Cys
    50                  55                  60

Gly Glu Leu Lys Lys Glu Lys Gly Ile His Arg Leu Glu Ala Met Leu
65                  70                  75                  80

Tyr Ala Ile Asp Gln Ile Asn Lys Asp Pro Asp Leu Leu Ser Asn Ile
                85                  90.                 95

Thr Leu Gly Val Arg Ile Leu Asp Thr Cys Ser Arg Asp Thr Tyr Ala
            100                 105                 110
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Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Glu Lys Asp Ala
115 120 125

Ser Asp Val Lys Cys Ala Asn Gly Asp Pro Pro Ile Phe Thr Lys Pro
130 135 140

Asp Lys Ile Ser Gly Val Ile Gly Ala Ala Ala Ser Ser Val Ser Ile
145 150 155 160

Met Val Ala Asn Ile Leu Arg Leu Phe Lys Ile Pro Gln Ile Ser Tyr
165 170 175

Ala Ser Thr Ala Pro Glu Leu Ser Asp Asn Thr Arg Tyr Asp Phe Phe
180 185 190

Ser Arg Val Val Pro Pro Asp Ser Tyr Gln Ala Gln Ala Met Val Asp
195 200 205

Ile Val Thr Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu Ala Ser Glu
210 215 220

Gly Asn Tyr Gly Glu Ser Gly Val Glu Ala Phe Thr Gln Ile Ser Arg
225 230 235 240

Glu Ile Gly Gly Val Cys Ile Ala Gln Ser Gln Lys Ile Pro Arg Glu
245 250 255

Pro Arg Pro Gly Glu Phe Glu Lys Ile Ile Lys Arg Leu Leu Glu Thr
260 265 270

Pro Asn Ala Arg Ala Val Ile Met Phe Ala Asn Glu Asp Asp Ile Arg
275 280 285

Arg Ile Leu Glu Ala Ala Lys Lys Leu Asn Gln Ser Gly His Phe Leu
290 295 300

Trp Ile Gly Ser Asp Ser Trp Gly Ser Lys Ile Ala Pro Val Tyr Gln
305 310 315 320

Gln Glu Glu Ile Ala Glu Gly Ala Val Thr Ile Leu Pro Lys Arg Ala
325 330 335

Ser Ile Asp Gly Phe Asp Arg Tyr Phe Arg Ser Arg Thr Leu Ala Asn
340 345 350

Asn Arg Arg Asn Val Trp Phe Ala Glu Phe Trp Glu Glu Asn Phe Gly
355 360 365

Cys Lys Leu Gly Ser His Gly Lys Arg Asn Ser His Ile Lys Lys Cys
370 375 380

Thr Gly Leu Glu Arg Ile Ala Arg Asp Ser Ser Tyr Glu Gln Glu Gly
385 390 395 400

Lys Val Gln Phe Val Ile Asp Ala Val Tyr Ser Met Ala Tyr Ala Leu
405 410 415

His Asn Met His Lys Asp Leu Cys Pro Gly Tyr Ile Gly Leu Cys Pro
420 425 430

Arg Met Ser Thr Ile Asp Gly Lys Glu Leu Leu Gly Tyr Ile Arg Ala
435 440 445

Val Asn Phe Asn Gly Ser Ala Gly Thr Pro Val Thr Phe Asn Glu Asn
450 455 460

Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe Gln Tyr Gln Ile Thr Asn
465 470 475 480

Lys Ser Thr Glu Tyr Lys Val Ile Gly His Trp Thr Asn Gln Leu His
485 490 495

Leu Lys Val Glu Asp Met Gln Trp Ala His Arg Glu His Thr His Pro
500 505 510

Ala Ser Val Cys Ser Leu Pro Cys Lys Pro Gly Glu Arg Lys Lys Thr
515 520 525

Val Lys Gly Val Pro Cys Cys Trp His Cys Glu Arg Cys Glu Gly Tyr
530 535 540

Asn Tyr Gln Val Asp Glu Leu Ser Cys Glu Leu Cys Pro Leu Asp Gln
545 550 555 560

Arg Pro Asn Met Asn Arg Thr Gly Cys Gln Leu Ile Pro Ile Ile Lys
565 570 575

Leu Glu Trp His Ser Pro Trp
580

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Gly Ile Ala Leu Thr Leu Phe Ala Val Leu Gly Ile Phe Leu Thr Ala
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Phe Val Leu Gly Val Phe Ile Lys Phe Arg Asn Thr Pro Ile Val Lys
20 25 30

Ala Thr Asn Arg Glu Leu Ser Tyr Leu Leu Leu Phe Ser Leu Leu Cys
35 40 45

Cys Phe Ser Ser Ser Leu Phe Phe Ile Gly Glu Pro Gln Asp Trp Thr
50 55 60

Cys Arg Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys Ile

65 70 75 80

Ser Cys Ile Leu Val Lys Thr Asn Arg Val Leu Leu Val Phe Glu Ala
85 90 95

Lys Ile Pro Thr Ser Phe His Arg Lys Trp Trp Gly Leu Asn Leu Gln
100 105 110

Phe Leu Leu Val Phe Leu Cys Thr Phe Met Gln Ile Val Ile Cys Val
115 120 125

Ile Trp Leu Tyr Thr Ala Pro Pro Ser Ser Tyr Arg Asn Gln Glu Leu
130 135 140

Glu Asp Glu Ile Ile Phe Ile Thr Cys His Glu Gly Ser Leu Met Ala
145 150 155 160

Leu Gly Phe Leu Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe
165 170 175

Phe Phe Ala Phe Lys Ser Arg Lys Leu Pro Glu Asn Phe Asn Glu Ala
180 185 190

Lys Phe Ile Thr Phe Ser Met Leu Ile Phe Phe Ile Val Trp Ile Ser
195 200 205

Phe Ile Pro Ala Tyr Ala Ser Thr Tyr Gly Lys Phe Val Ser Ala Val
210 215 220

Glu Val Ile Ala Ile Leu Ala Ala Ser Phe Gly Leu Leu Ala Cys Ile
225 230 235 240

Phe Phe Asn Lys Ile Tyr Ile Ile Leu Phe
245 250

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1 5 10 15

Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile
20 25 30

Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser
35 40 45

Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile
50 55 60

Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu
65 70 75 80

Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp
85 90 95

Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg
100 105 110

Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val
115 120 125

Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu
130 135 140

His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile
145 150 155 160

Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met
165 170 175

Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu
180 185 190

Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys
195 200 205

Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val
210 215 220

Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln
225 230 235 240

Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr
245 250 255

Ile Thr Leu Val Val Leu Phe Val Pro Lys Met
260 265

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Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala
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Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile
20 25 30

Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser
35 40 45

Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile
    50   55   60

Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu
65   70   75   80

Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp
                85   90   95

Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg
            100   105   110

Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val
        115   120   125

Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu
    130   135   140

His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile
145   150   155   160

Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met
                165   170   175

Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu
            180   185   190

Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys
        195   200   205

Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val
    210   215   220

Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln
225   230   235   240

Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr
                245   250   255

Ile Thr Leu Val Val Leu Phe Val Pro Lys Met
            260   265

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<400> 9

Leu Tyr Ser Ile Leu Ser Ala Leu Thr Ile Leu Gly Met Ile Met Ala
1   5   10   15

Ser Ala Phe Leu Phe Phe Asn Ile Lys Asn Arg Asn Gln Lys Leu Ile
20 25 30

Lys Met Ser Ser Pro Tyr Met Asn Asn Leu Ile Ile Leu Gly Gly Met
35 40 45

Leu Ser Tyr Ala Ser Ile Phe Leu Phe Gly Leu Asp Gly Ser Phe Val
50 55 60

Ser Glu Lys Thr Phe Glu Thr Leu Cys Thr Val Arg Thr Trp Ile Leu
65 70 75 80

Thr Val Gly Tyr Thr Thr Ala Phe Gly Ala Met Phe Ala Lys Thr Trp
85 90 95

Arg Val His Ala Ile Phe Lys Asn Val Lys Met Lys Lys Lys Ile Ile
100 105 110

Lys Asp Gln Lys Leu Leu Val Ile Val Gly Gly Met Leu Leu Ile Asp
115 120 125

Leu Cys Ile Leu Ile Cys Trp Gln Ala Val Asp Pro Leu Arg Arg Thr
130 135 140

Val Glu Lys Tyr Ser Met Glu Pro Asp Pro Ala Gly Arg Asp Ile Ser
145 150 155 160

Ile Arg Pro Leu Leu Glu His Cys Glu Asn Thr His Met Thr Ile Trp
165 170 175

Leu Gly Ile Val Tyr Ala Tyr Lys Gly Leu Leu Met Leu Phe Gly Cys
180 185 190

Phe Leu Ala Trp Glu Thr Arg Asn Val Ser Ile Pro Ala Leu Asn Asp
195 200 205

Ser Lys Tyr Ile Gly Met Ser Val Tyr Asn Val Gly Ile Met Cys Ile
210 215 220

Ile Gly Ala Ala Val Ser Phe Leu Thr Arg Asp Gln Pro Asn Val Gln
225 230 235 240

Phe Cys Ile Val Ala Leu Val Ile Ile Phe Cys Ser Thr Ile Thr Leu
245 250 255

Cys Leu Val Phe Val Pro Lys Leu
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<210> 10
<211> 260
<212> PRT
<213> Human

<400> 10

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Phe Val Ile Val Thr Phe Val Arg Tyr Asn Asp Thr Pro Ile Val Arg
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Ala Ser Gly Arg Glu Leu Ser Tyr Val Leu Leu Thr Gly Ile Phe Leu
        35                  40                  45

Cys Tyr Ser Ile Thr Phe Leu Met Ile Ala Ala Pro Asp Thr Ile Ile
    50                  55                  60

Cys Ser Phe Arg Arg Val Phe Leu Gly Leu Gly Met Cys Phe Ser Tyr
65                  70                  75                  80

Ala Ala Leu Leu Thr Lys Thr Asn Arg Ile His Arg Ile Phe Glu Gln
                85                  90                  95

Gly Lys Lys Ser Val Thr Ala Pro Lys Phe Ile Ser Pro Ala Ser Gln
            100                 105                 110

Leu Val Ile Thr Phe Ser Leu Ile Ser Val Gln Leu Leu Gly Val Phe
        115                 120                 125

Val Trp Phe Val Val Asp Pro Pro His Ile Ile Ile Asp Tyr Gly Glu
    130                 135                 140

Gln Arg Thr Leu Asp Pro Glu Lys Ala Arg Gly Val Leu Lys Cys Asp
145                 150                 155                 160

Ile Ser Asp Leu Ser Leu Ile Cys Ser Leu Gly Tyr Ser Ile Leu Leu
                165                 170                 175


Met Val Thr Cys Thr Val Tyr Ala Ile Lys Thr Arg Gly Val Pro Glu
            180                 185                 190

Thr Phe Asn Glu Ala Lys Pro Ile Gly Phe Thr Met Tyr Thr Thr Cys
        195                 200                 205

Ile Ile Trp Leu Ala Phe Ile Pro Ile Phe Phe Gly Thr Ala Gln Ser
    210                 215                 220

Ala Glu Lys Met Tyr Ile Gln Thr Thr Thr Leu Thr Val Ser Met Ser
225                 230                 235                 240

Leu Ser Ala Ser Val Ser Leu Gly Met Leu Tyr Met Pro Lys Val Tyr
                245                 250                 255

Ile Ile Ile Phe
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<400> 11

Lys Pro Ser Arg Asn Thr Ile Glu Glu Val Arg Cys Ser Thr Ala Ala
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His Ala Phe Lys Val Ala Ala Arg Ala Thr Leu Arg Arg Ser Asn Val
            20   25   30

Ser Arg Lys Arg Ser Ser Ser Leu Gly Gly Ser Thr Gly Ser Thr Pro
        35   40   45

Ser Ser Ser Ile Ser Ser Lys Ser Asn Ser Glu Asp Pro Phe Pro Gln
    50   55   60

Pro Glu Arg Gln Lys Gln Gln Gln Pro Leu Ala Leu Thr Gln Gln Glu
65   70   75   80

Gln Gln Gln Gln Pro Leu Thr Leu Pro Gln Gln Gln Arg Ser Gln Gln
                85   90   95

Gln Pro Arg Cys Lys Gln Lys Val Ile Phe Gly Ser Gly Thr Val Thr
            100   105   110

Phe Ser Leu Ser Phe Asp Glu Pro Gln Lys Asn Ala Met Ala His Gly
        115   120   125

Asn Ser Thr His Gln Asn Ser Leu Glu Ala Gln Lys Ser Ser Asp Thr
    130   135   140

Leu Thr Arg His Gln Pro Leu Leu Pro Leu Gln Cys Gly Glu Thr Asp
145   150   155   160

Leu Asp Leu Thr Val Gln Glu Thr Gly Leu Gln Gly Pro Val Gly Gly
                165   170   175

Asp Gln Arg Pro Glu Val Glu Asp Pro Glu Glu Leu Ser Pro Ala Leu
            180   185   190

Val Val Ser Ser Ser Gln Ser Phe Val Ile Ser Gly Gly Gly Ser Thr
        195   200   205

Val Thr Glu Asn Val Val Asn Ser
    210   215

<210> 12
<211> 104
<212> PRT
<213> Human

<400> 12

Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr
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Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg
            20   25   30

Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys
        35   40   45

Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln
    50   55   60

Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly
65   70   75   80

Leu Pro Arg Gly Pro Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly
                85   90   95

Ser Arg Val His Leu Leu Tyr Lys
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<210> 13
<211> 104
<212> PRT
<213> Human

<400> 13

Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr
1   5   10   15

Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg
            20   25   30

Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys
        35   40   45

Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln
    50   55   60

Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly
65   70   75   80

Leu Pro Arg Gly Pro Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly
                85   90   95

Ser Arg Val His Leu Leu Tyr Lys
            100

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<211> 197
<212> PRT
<213> Human

<400> 14

Ile Thr Leu Arg Thr Asn Pro Asp Ala Ala Thr Gln Asn Arg Arg Phe
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Gln Phe Thr Gln Asn Gln Lys Lys Glu Asp Ser Lys Thr Ser Thr Ser
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Val Thr Ser Val Asn Gln Ala Ser Thr Ser Arg Leu Glu Gly Leu Gln
35 40 45

Ser Glu Asn His Arg Leu Arg Met Lys Ile Thr Glu Leu Asp Lys Asp
50 55 60

Leu Glu Glu Val Thr Met Gln Leu Gln Asp Thr Pro Glu Lys Thr Thr
65 70 75 80

Tyr Ile Lys Gln Asn His Tyr Gln Glu Leu Asn Asp Ile Leu Asn Leu
85 90 95

Gly Asn Phe Thr Glu Ser Thr Asp Gly Gly Lys Ala Ile Leu Lys Asn
100 105 110

His Leu Asp Gln Asn Pro Gln Leu Gln Trp Asn Thr Thr Glu Pro Ser
115 120 125

Arg Thr Cys Lys Asp Pro Ile Glu Asp Ile Asn Ser Pro Glu His Ile
130 135 140

Gln Arg Arg Leu Ser Leu Gln Leu Pro Ile Leu His His Ala Tyr Leu
145 150 155 160

Pro Ser Ile Gly Gly Val Asp Ala Ser Cys Val Ser Pro Cys Val Ser
165 170 175

Pro Thr Ala Ser Pro Arg His Arg His Val Pro Pro Ser Phe Arg Val
180 185 190

Met Val Ser Gly Leu
195

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<400> 15

His Pro Glu Gln Asn Val Gln Lys Arg Lys Arg Ser Phe Lys Ala Val
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Val Thr Ala Ala Thr Met Gln Ser Lys Leu Ile Gln Lys Gly Asn Asp
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Arg Pro Asn Gly Glu Val Lys Ser Glu Leu Cys Glu Ser Leu Glu Thr
35 40 45

Asn Ser Lys Ser Ser Val Glu Phe Pro Met Val Lys Ser Gly Ser Thr
50 55 60

Ser
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<210> 16
<211> 374
<212> PRT
<213> Human

<400> 16

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Glu Glu Lys Thr Ala Ala Arg Ile Asp Gln Glu Ile Asn Arg Ile Leu
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Leu Glu Gln Lys Lys Gln Glu Arg Glu Glu Leu Lys Leu Leu Leu Leu
35 40 45

Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
50 55 60

Ile His Gly Val Gly Tyr Ser Glu Glu Asp Arg Arg Ala Phe Arg Leu
65 70 75 80

Leu Ile Tyr Gln Asn Ile Phe Val Ser Met Gln Ala Met Ile Asp Ala
85 90 95

Met Asp Arg Leu Gln Ile Pro Phe Ser Arg Pro Asp Ser Lys Gln His
100 105 110

Ala Ser Leu Val Met Thr Gln Asp Pro Tyr Lys Val Ser Thr Phe Glu
115 120 125

Lys Pro Tyr Ala Val Ala Met Gln Tyr Leu Trp Arg Asp Ala Gly Ile
130 135 140

Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala
145 150 155 160

Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Ser Glu Asp Ser Tyr Ile
165 170 175

Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile
180 185 190

Asn Glu Tyr Cys Phe Ser Val Lys Lys Thr Lys Leu Arg Ile Val Asp
195 200 205

Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe Glu
210 215 220

Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln
225 230 235 240

Cys Leu Glu Glu Asn Asp Gln Glu Asn Arg Met Glu Glu Ser Leu Ala
245 250 255

Leu Phe Ser Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val
260 265 270

Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Asp Lys Ile His Thr
275 280 285

Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Arg Arg Asp
290 295 300

Ala Glu Ala Ala Lys Ser Phe Ile Leu Asp Met Tyr Ala Arg Val Tyr
305 310 315 320

Ala Ser Cys Ala Glu Pro Gln Asp Gly Gly Arg Lys Gly Ser Arg Ala
325 330 335

Arg Arg Phe Phe Ala His Phe Thr Cys Ala Thr Asp Thr Gln Ser Val
340 345 350

Arg Ser Val Phe Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu
355 360 365

Asp Glu Ile Asn Leu Leu
370

<210> 17
<211> 374
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<400> 17

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Asp Glu Lys Ala Ala Ala Arg Val Asp Gln Glu Ile Asn Arg Ile Leu
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Leu Glu Gln Lys Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu Leu
35 40 45

Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
50 55 60

Ile His Gly Ala Gly Tyr Ser Glu Glu Glu Arg Lys Gly Phe Arg Pro
65 70 75 80

Leu Val Tyr Gln Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala
85 90 95

Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu Ser Lys His His
100 105 110

Ala Ser Leu Val Met Ser Gln Asp Pro Tyr Lys Val Thr Thr Phe Glu
115 120 125

Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile
130 135 140

Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala
145 150 155 160

Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val
165 170 175

Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile
180 185 190

Asn Glu Tyr Cys Phe Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp
195 200 205

Val Gly Gly Gln Lys Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu
210 215 220

Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln
225 230 235 240

Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys Glu Ser Leu Ala
245 250 255

Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val
260 265 270

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Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr
        275                 280                 285

Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp
    290                 295                 300

Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr
305                 310                 315                 320

Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Lys Lys Gly Ala Arg Ser
                325                 330                 335

Arg Arg Leu Phe Ser His Tyr Thr Cys Ala Thr Asp Thr Gln Asn Ile
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Asp Glu Ile Asn Leu Leu
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<211> 3464
<212> DNA
<213> Human

<400> 19

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<212> DNA
<213> Human

<400> 20

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Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu
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Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp
705 710 715 720

Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr
725 730 735

Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser
740 745 750

Ile Leu Pro Gln Leu Glu His Cys Ser Ser Lys Lys Met Asn Thr Trp
755 760 765

Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly Ile
770 775 780

Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp
785 790 795 800

His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu
805 810 815

Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala
820 825 830

Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu
835 840 845

Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu
850 855 860

Trp Gln Ser Glu Thr Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn

865 870 875 880

Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu
885 890 895

Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg
900 905 910

His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro
915 920 925

Thr Pro Pro Asp Pro Ser Gly Gly Leu Pro Arg Gly Pro Ser Glu Pro
930 935 940

Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys
945 950 955 960

<210> 25
<211> 844
<212> PRT
<213> Rat

<400> 25

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Pro His Leu Pro Arg Pro His Pro Arg Val Pro Pro His Pro Ser Ser
35 40 45

Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly
50 55 60

Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu
65 70 75 80

Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu
85 90 95

Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu
100 105 110

Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly
115 120 125

Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn
130 135 140

Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg
145 150 155 160

Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His

165 170 175

Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile
180 185 190

Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp
195 200 205

Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln
210 215 220

Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln
225 230 235 240

Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys
245 250 255

Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val
260 265 270

Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Thr Tyr Asp
275 280 285

Pro Ser Ile Asn Cys Thr Val Glu Glu Met Thr Glu Ala Val Glu Gly
290 295 300

His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser
305 310 315 320

Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg
325 330 335

Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu
340 345 350

Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser
355 360 365

Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn
370 375 380

Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser
385 390 395 400

Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg
405 410 415

Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys
420 425 430

Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr
435 440 445

Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln Ile Leu Val Ile
450 455 460

Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile Ser Val Ser Val
465 470 475 480

Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys Leu Ser Phe Asn
485 490 495

Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu
500 505 510

Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu Ala Ala Val Phe
515 520 525

Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Ser Gln Phe Pro Phe
530 535 540

Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly
545 550 555 560

Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His Thr Val Phe Thr
565 570 575

Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys
580 585 590

Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp Val Leu Thr Leu
595 600 605

Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr Ile Glu Thr Phe
610 615 620

Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser Ile Leu Pro Gln
625 630 635 640

Leu Glu His Cys Ser Ser Lys Lys Met Asn Thr Trp Leu Gly Ile Phe
645 650 655

Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr
660 665 670

Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp His Arg Ala Val
675 680 685

Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu Ile Thr Ala Pro
690 695 700

Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala
705 710 715 720

Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu Val Val Leu Phe
725 730 735

Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu
740 745 750

Thr Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu

755 760 765

Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile
770 775 780

Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln
785 790 795 800

Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Asp
805 810 815

Pro Ser Gly Gly Leu Pro Arg Gly Pro Ser Glu Pro Pro Asp Arg Leu
820 825 830

Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys
835 840

<210> 26
<211> 2616
<212> DNA
<213> Human

<400> 26

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caccagaagg gcggcccagc agaggactgt ggtcctgtca atgagcaccg tggcatccag     180
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<210> 27
<211> 824
<212> PRT
<213> Human

<400> 27

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Val Leu Gly Gly Leu Phe Pro Val His Gln Lys Gly Gly Pro Ala Glu
        35                  40                  45

Asp Cys Gly Pro Val Asn Glu His Arg Gly Ile Gln Arg Leu Glu Ala
    50                  55                  60

Met Leu Phe Ala Leu Asp Arg Ile Asn Arg Asp Pro His Leu Leu Pro
65                  70                  75                  80

Gly Val Arg Leu Gly Ala His Ile Leu Asp Ser Cys Ser Lys Asp Thr
                85                  90                  95

His Ala Leu Glu Gln Ala Leu Asp Phe Val Arg Ala Ser Leu Ser Arg
            100                 105                 110

Gly Ala Asp Gly Ser Arg His Ile Cys Pro Asp Gly Ser Tyr Ala Thr
        115                 120                 125

His Gly Asp Ala Pro Thr Ala Ile Thr Gly Val Ile Gly Gly Ser Tyr
    130                 135                 140

Ser Asp Val Ser Ile Gln Val Ala Asn Leu Leu Arg Leu Phe Gln Ile
145                 150                 155                 160

Pro Gln Ile Ser Tyr Ala Ser Thr Ser Ala Lys Leu Ser Asp Lys Ser
                165                 170                 175

Arg Tyr Asp Tyr Phe Ala Arg Thr Val Pro Pro Asp Phe Phe Gln Ala
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180 185 190

Lys Ala Met Ala Glu Ile Leu Arg Phe Phe Asn Trp Thr Tyr Val Ser
195 200 205

Thr Glu Ala Ser Glu Gly Asp Tyr Gly Glu Thr Gly Ile Glu Ala Phe
210 215 220

Glu Leu Glu Ala Arg Ala Arg Asn Ile Cys Val Ala Thr Ser Glu Lys
225 230 235 240

Val Gly Arg Ala Met Ser Arg Ala Ala Phe Glu Gly Val Val Arg Ala
245 250 255

Leu Leu Gln Lys Pro Ser Ala Arg Val Ala Val Leu Phe Thr Arg Ser
260 265 270

Glu Asp Ala Arg Glu Leu Leu Ala Ala Ser Gln Arg Leu Asn Ala Ser
275 280 285

Phe Thr Trp Val Ala Ser Asp Gly Trp Gly Ala Leu Glu Ser Val Val
290 295 300

Ala Gly Ser Glu Gly Ala Ala Glu Gly Ala Ile Thr Ile Glu Leu Ala
305 310 315 320

Ser Tyr Pro Ile Ser Asp Phe Ala Ser Tyr Phe Gln Ser Leu Asp Pro
325 330 335

Trp Asn Asn Ser Arg Asn Pro Trp Phe Arg Glu Phe Trp Glu Gln Arg
340 345 350

Phe Arg Cys Ser Phe Arg Gln Arg Asp Cys Ala Ala His Ser Leu Arg
355 360 365

Ala Val Pro Phe Glu Gln Glu Ser Lys Ile Met Phe Val Val Asn Ala
370 375 380

Val Tyr Ala Met Ala His Ala Leu His Asn Met His Arg Ala Leu Cys
385 390 395 400

Pro Asn Thr Thr Arg Leu Cys Asp Ala Met Arg Pro Val Asn Gly Arg
405 410 415

Arg Leu Tyr Lys Asp Phe Val Leu Asn Val Lys Phe Asp Ala Pro Phe
420 425 430

Arg Pro Ala Asp Thr His Asn Glu Val Arg Phe Asp Arg Phe Gly Asp
435 440 445

Gly Ile Gly Arg Tyr Asn Ile Phe Thr Tyr Leu Arg Ala Gly Ser Gly
450 455 460

Arg Tyr Arg Tyr Gln Lys Val Gly Tyr Trp Ala Glu Gly Leu Thr Leu
465 470 475 480

Asp Thr Ser Leu Ile Pro Trp Ala Ser Pro Ser Ala Gly Pro Leu Ala

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                485                 490                 495

Ala Ser Arg Cys Ser Glu Pro Cys Leu Gln Asn Glu Val Lys Ser Val
            500                 505                 510

Gln Pro Gly Glu Val Cys Cys Trp Leu Cys Ile Pro Cys Gln Pro Tyr
        515                 520                 525

Glu Tyr Arg Leu Asp Glu Phe Thr Cys Ala Asp Cys Gly Leu Gly Tyr
    530                 535                 540

Trp Pro Asn Ala Ser Leu Thr Gly Cys Phe Glu Leu Pro Gln Glu Tyr
545                 550                 555                 560

Ile Arg Trp Gly Asp Ala Trp Ala Val Gly Pro Val Thr Ile Ala Cys
                565                 570                 575

Leu Gly Ala Leu Ala Thr Leu Phe Val Leu Gly Val Phe Val Arg His
            580                 585                 590

Asn Ala Thr Pro Val Val Lys Ala Ser Gly Arg Glu Leu Cys Tyr Ile
        595                 600                 605

Leu Leu Gly Gly Val Phe Leu Cys Tyr Cys Met Thr Phe Ile Phe Ile
    610                 615                 620

Ala Lys Pro Ser Thr Ala Val Cys Thr Leu Arg Arg Leu Gly Leu Gly
625                 630                 635                 640

Thr Ala Phe Ser Val Cys Tyr Ser Ala Leu Leu Thr Lys Thr Asn Arg
                645                 650                 655

Ile Ala Arg Ile Phe Gly Gly Ala Arg Glu Gly Ala Gln Arg Pro Arg
            660                 665                 670

Phe Ile Ser Pro Ala Ser Gln Val Ala Ile Cys Leu Ala Leu Ile Ser
        675                 680                 685

Gly Gln Leu Leu Ile Val Val Ala Trp Leu Val Val Glu Ala Pro Gly
    690                 695                 700

Thr Gly Lys Glu Thr Ala Pro Glu Arg Arg Glu Val Val Thr Leu Arg
705                 710                 715                 720

Cys Asn His Arg Asp Ala Ser Met Leu Gly Ser Leu Ala Tyr Asn Val
                725                 730                 735

Leu Leu Ile Ala Leu Cys Thr Leu Tyr Ala Phe Asn Thr Arg Lys Cys
            740                 745                 750

Pro Glu Asn Phe Asn Glu Ala Lys Phe Ile Gly Phe Thr Met Tyr Thr
        755                 760                 765

Thr Cys Ile Ile Trp Leu Ala Leu Leu Pro Ile Phe Tyr Val Thr Ser
    770                 775                 780
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Ser Asp Tyr Arg Val Gln Thr Thr Thr Met Cys Val Ser Val Ser Leu
785 790 795 800

Ser Gly Ser Val Val Leu Gly Cys Leu Phe Ala Pro Lys Leu His Ile
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Ile Leu Phe Gln Pro Gln Lys Asn
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<210> 28
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Gqi5

<400> 28

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gacaaaatta tctactccca cttcacgtgc gccacagaca ccgagaatat ccgctttgtc    1020
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<213> Artificial Sequence

<220>
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<400> 29

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20 25 30

Lys Arg Asp Ala Arg Arg Glu Leu Lys Leu Leu Leu Leu Gly Thr Gly

35 40 45

Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile Ile His Gly
50 55 60

Ser Gly Tyr Ser Asp Glu Asp Lys Arg Gly Phe Thr Lys Leu Val Tyr
65 70 75 80

Gln Asn Ile Phe Thr Ala Met Gln Ala Met Ile Arg Ala Met Asp Thr
85 90 95

Leu Lys Ile Pro Tyr Lys Tyr Glu His Asn Lys Ala His Ala Gln Leu
100 105 110

Val Arg Glu Val Asp Val Glu Lys Val Ser Ala Phe Glu Asn Pro Tyr
115 120 125

Val Asp Ala Ile Lys Ser Leu Trp Asn Asp Pro Gly Ile Gln Glu Cys
130 135 140

Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser Asp Ser Thr Lys Tyr Tyr
145 150 155 160

Leu Asn Asp Leu Asp Arg Val Ala Asp Pro Ala Tyr Leu Pro Thr Gln
165 170 175

Gln Asp Val Leu Arg Val Arg Val Pro Thr Thr Gly Ile Ile Glu Tyr
180 185 190

Pro Phe Asp Leu Gln Ser Val Ile Phe Arg Met Val Asp Val Gly Gly
195 200 205

Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe Glu Asn Val Thr
210 215 220

Ser Ile Met Phe Leu Val Ala Leu Ser Glu Tyr Asp Gln Val Leu Val
225 230 235 240

Glu Ser Asp Asn Glu Asn Arg Met Glu Glu Ser Lys Ala Leu Phe Arg
245 250 255

Thr Ile Ile Thr Tyr Pro Trp Phe Gln Asn Ser Ser Val Ile Leu Phe
260 265 270

Leu Asn Lys Lys Asp Leu Leu Glu Glu Lys Ile Met Tyr Ser His Leu
275 280 285

Val Asp Tyr Phe Pro Glu Tyr Asp Gly Pro Gln Arg Asp Ala Gln Ala
290 295 300

Ala Arg Glu Phe Ile Leu Lys Met Phe Val Asp Leu Asn Pro Asp Ser
305 310 315 320

Asp Lys Ile Ile Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn
325 330 335

Ile Arg Phe Val Phe Ala Ala Val Lys Asp Thr Ile Leu Gln Leu Asn

340 345 350

Leu Lys Asp Cys Gly Leu Phe
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<211> 2751
<212> DNA
<213> Artificial Sequence

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<223> Chimeric hCAR/hmGluR2

<400> 30

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<400> 31

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20 25 30

Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Ala Lys Asp
35 40 45

Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys Ile Arg Tyr Asn
50 55 60

Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe Ala Ile Glu Glu
65 70 75 80

Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Leu Thr Leu Gly Tyr Arg
85 90 95

Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu Glu Ala Thr Leu
100 105 110

Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn Leu Asp Glu Phe
115 120 125

Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala Val Val Gly Ala
130 135 140

Thr Gly Ser Gly Val Ser Thr Ala Val Ala Asn Leu Leu Gly Leu Phe
145 150 155 160

Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg Leu Leu Ser Asn
165 170 175

Lys Asn Gln Phe Lys Ser Phe Leu Arg Thr Ile Pro Asn Asp Glu His
180 185 190

Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe Arg Trp Asn Trp
195 200 205

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Val Gly Thr Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly Ile Glu
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Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys Ile Asp Phe Ser
225                 230                 235                 240

Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Glu Ile Gln His Val Val
                245                 250                 255

Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val Val Phe Ser Ser
            260                 265                 270

Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val Arg Arg Asn Ile
        275                 280                 285

Thr Gly Lys Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser Ser Leu
    290                 295                 300

Ile Ala Met Pro Gln Tyr Phe His Val Val Gly Gly Thr Ile Gly Phe
305                 310                 315                 320

Ala Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu Phe Leu Lys Lys
                325                 330                 335

Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala Lys Glu Phe Trp
            340                 345                 350

Glu Glu Thr Phe Asn Cys His Leu Gln Glu Gly Ala Lys Gly Pro Leu
        355                 360                 365

Pro Val Asp Thr Phe Leu Arg Gly His Glu Glu Ser Gly Asp Arg Phe
    370                 375                 380

Ser Asn Ser Ser Thr Ala Phe Arg Pro Leu Cys Thr Gly Asp Glu Asn
385                 390                 395                 400

Ile Ser Ser Val Glu Thr Pro Tyr Ile Asp Tyr Thr His Leu Arg Ile
                405                 410                 415

Ser Tyr Asn Val Tyr Leu Ala Val Tyr Ser Ile Ala His Ala Leu Gln
            420                 425                 430

Asp Ile Tyr Thr Cys Leu Pro Gly Arg Gly Leu Phe Thr Asn Gly Ser
        435                 440                 445

Cys Ala Asp Ile Lys Lys Val Glu Ala Trp Gln Val Leu Lys His Leu
    450                 455                 460

Arg His Leu Asn Phe Thr Asn Asn Met Gly Glu Gln Val Thr Phe Asp
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Glu Cys Gly Asp Leu Val Gly Asn Tyr Ser Ile Ile Asn Trp His Leu
                485                 490                 495
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Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val Gly Tyr Tyr Asn
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Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn Glu Glu Lys Ile
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Leu Trp Ser Gly Phe Ser Arg Glu Val Pro Phe Ser Asn Cys Ser Arg
    530                 535                 540

Asp Cys Leu Ala Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr
545                 550                 555                 560

Cys Cys Phe Glu Cys Val Glu Cys Pro Asp Gly Glu Tyr Ser Asp Glu
                565                 570                 575

Thr Asp Ala Ser Ala Cys Asn Lys Cys Pro Asp Asp Phe Trp Ser Asn
            580                 585                 590

Glu Asn His Thr Ser Cys Phe Glu Leu Pro Gln Glu Tyr Ile Arg Trp
        595                 600                 605

Gly Asp Ala Trp Ala Val Gly Pro Val Thr Ile Ala Cys Leu Gly Ala
    610                 615                 620

Leu Ala Thr Leu Phe Val Leu Gly Val Phe Val Arg His Asn Ala Thr
625                 630                 635                 640

Pro Val Val Lys Ala Ser Gly Arg Glu Leu Cys Tyr Ile Leu Leu Gly
                645                 650                 655

Gly Val Phe Leu Cys Tyr Cys Met Thr Phe Ile Phe Ile Ala Lys Pro
            660                 665                 670

Ser Thr Ala Val Cys Thr Leu Arg Arg Leu Gly Leu Gly Thr Ala Phe
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Ser Val Cys Tyr Ser Ala Leu Leu Thr Lys Thr Asn Arg Ile Ala Arg
    690                 695                 700

Ile Phe Gly Gly Ala Arg Glu Gly Ala Gln Arg Pro Arg Phe Ile Ser
705                 710                 715                 720

Pro Ala Ser Gln Val Ala Ile Cys Leu Ala Leu Ile Ser Gly Gln Leu
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Leu Ile Val Val Ala Trp Leu Val Val Glu Ala Pro Gly Thr Gly Lys
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Glu Thr Ala Pro Glu Arg Arg Glu Val Val Thr Leu Arg Cys Asn His
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Arg Asp Ala Ser Met Leu Gly Ser Leu Ala Tyr Asn Val Leu Leu Ile
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Ala Leu Cys Thr Leu Tyr Ala Phe Asn Thr Arg Lys Cys Pro Glu Asn
785                 790                 795                 800
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Phe Asn Glu Ala Lys Phe Ile Gly Phe Thr Met Tyr Thr Thr Cys Ile
805 810 815

Ile Trp Leu Ala Leu Leu Pro Ile Phe Tyr Val Thr Ser Ser Asp Tyr
820 825 830

Arg Val Gln Thr Thr Thr Met Cys Val Ser Val Ser Leu Ser Gly Ser
835 840 845

Val Val Leu Gly Cys Leu Phe Ala Pro Lys Leu His Ile Ile Leu Phe
850 855 860

Gln Pro Gln Lys Asn Val Val Ser His Arg Ala Pro Thr Ser Arg Phe
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Gly Ser Ala Ala Ala Arg Ala Ser Ser Ser Leu Gly Gln Gly Ser Gly
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Thr Thr Ser Ser Leu
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<223> Chimeric phCaR/hmGluR2*Gqi5

<400> 33

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Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Ala Lys Asp
        35                  40                  45

Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys Ile Arg Tyr Asn
    50                  55                  60

Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe Ala Ile Glu Glu
65                  70                  75                  80

Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Leu Thr Leu Gly Tyr Arg
                85                  90                  95

Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu Glu Ala Thr Leu
            100                 105                 110

Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn Leu Asp Glu Phe
        115                 120                 125

Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala Val Val Gly Ala
    130                 135                 140

Thr Gly Ser Gly Val Ser Thr Ala Val Ala Asn Leu Leu Gly Leu Phe
145                 150                 155                 160

Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg Leu Leu Ser Asn
                165                 170                 175

Lys Asn Gln Phe Lys Ser Phe Leu Arg Thr Ile Pro Asn Asp Glu His
            180                 185                 190

Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe Arg Trp Asn Trp
        195                 200                 205

Val Gly Thr Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly Ile Glu
    210                 215                 220

Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys Ile Asp Phe Ser
225                 230                 235                 240

Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Glu Ile Gln His Val Val
                245                 250                 255
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Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val Val Phe Ser Ser
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Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val Arg Arg Asn Ile
275 280 285

Thr Gly Lys Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser Ser Leu
290 295 300

Ile Ala Met Pro Gln Tyr Phe His Val Val Gly Gly Thr Ile Gly Phe
305 310 315 320

Ala Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu Phe Leu Lys Lys
325 330 335

Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala Lys Glu Phe Trp
340 345 350

Glu Glu Thr Phe Asn Cys His Leu Gln Glu Gly Ala Lys Gly Pro Leu
355 360 365

Pro Val Asp Thr Phe Leu Arg Gly His Glu Glu Ser Gly Asp Arg Phe
370 375 380

Ser Asn Ser Ser Thr Ala Phe Arg Pro Leu Cys Thr Gly Asp Glu Asn
385 390 395 400

Ile Ser Ser Val Glu Thr Pro Tyr Ile Asp Tyr Thr His Leu Arg Ile
405 410 415

Ser Tyr Asn Val Tyr Leu Ala Val Tyr Ser Ile Ala His Ala Leu Gln
420 425 430

Asp Ile Tyr Thr Cys Leu Pro Gly Arg Gly Leu Phe Thr Asn Gly Ser
435 440 445

Cys Ala Asp Ile Lys Lys Val Glu Ala Trp Gln Val Leu Lys His Leu
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Arg His Leu Asn Phe Thr Asn Asn Met Gly Glu Gln Val Thr Phe Asp
465 470 475 480

Glu Cys Gly Asp Leu Val Gly Asn Tyr Ser Ile Ile Asn Trp His Leu
485 490 495

Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val Gly Tyr Tyr Asn
500 505 510

Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn Glu Glu Lys Ile
515 520 525

Leu Trp Ser Gly Phe Ser Arg Glu Val Pro Phe Ser Asn Cys Ser Arg
530 535 540

Asp Cys Leu Ala Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr

545 550 555 560

Cys Cys Phe Glu Cys Val Glu Cys Pro Asp Gly Glu Tyr Ser Asp Glu
565 570 575

Thr Asp Ala Ser Ala Cys Asn Lys Cys Pro Asp Asp Phe Trp Ser Asn
580 585 590

Glu Asn His Thr Ser Cys Phe Glu Leu Pro Gln Glu Tyr Ile Arg Trp
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Gly Asp Ala Trp Ala Val Gly Pro Val Thr Ile Ala Cys Leu Gly Ala
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Leu Ala Thr Leu Phe Val Leu Gly Val Phe Val Arg His Asn Ala Thr
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Pro Val Val Lys Ala Ser Gly Arg Glu Leu Cys Tyr Ile Leu Leu Gly
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Gly Val Phe Leu Cys Tyr Cys Met Thr Phe Ile Phe Ile Ala Lys Pro
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Ser Thr Ala Val Cys Thr Leu Arg Arg Leu Gly Leu Gly Thr Ala Phe
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Ser Val Cys Tyr Ser Ala Leu Leu Thr Lys Thr Asn Arg Ile Ala Arg
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Pro Ala Ser Gln Val Ala Ile Cys Leu Ala Leu Ile Ser Gly Gln Leu
725 730 735

Leu Ile Val Val Ala Trp Leu Val Val Glu Ala Pro Gly Thr Gly Lys
740 745 750

Glu Thr Ala Pro Glu Arg Arg Glu Val Val Thr Leu Arg Cys Asn His
755 760 765

Arg Asp Ala Ser Met Leu Gly Ser Leu Ala Tyr Asn Val Leu Leu Ile
770 775 780

Ala Leu Cys Thr Leu Tyr Ala Phe Asn Thr Arg Lys Cys Pro Glu Asn
785 790 795 800

Phe Asn Glu Ala Lys Phe Ile Gly Phe Thr Met Tyr Thr Thr Cys Ile
805 810 815

Ile Trp Leu Ala Leu Leu Pro Ile Phe Tyr Val Thr Ser Ser Asp Tyr
820 825 830

Arg Val Gln Thr Thr Thr Met Cys Val Ser Val Ser Leu Ser Gly Ser
835 840 845

Val Val Leu Gly Cys Leu Phe Ala Pro Lys Leu His Ile Ile Leu Phe
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Gln Pro Gln Lys Asn Val Val Ser His Arg Ala Pro Thr Ser Arg Phe
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Gly Ser Ala Ala Ala Arg Ala Ser Ser Ser Leu Gly Gln Gly Ser Gly
                885   890   895

Ser Gln Phe Val Pro Thr Val Cys Asn Gly Arg Glu Val Val Asp Ser
            900   905   910

Thr Thr Ser Ser Leu Met Thr Leu Glu Ser Ile Met Ala Cys Cys Leu
        915   920   925

Ser Glu Glu Ala Lys Glu Ala Arg Arg Ile Asn Asp Glu Ile Glu Arg
    930   935   940

Gln Leu Arg Arg Asp Lys Arg Asp Ala Arg Arg Glu Leu Lys Leu Leu
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Leu Leu Gly Thr Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met
                965   970   975

Arg Ile Ile His Gly Ser Gly Tyr Ser Asp Glu Asp Lys Arg Gly Phe
            980   985   990

Thr Lys Leu Val Tyr Gln Asn Ile Phe Thr Ala Met Gln Ala Met Ile
        995   1000   1005

Arg Ala Met Asp Thr Leu Lys Ile Pro Tyr Lys Tyr Glu His Asn Lys
    1010   1015   1020

Ala His Ala Gln Leu Val Arg Glu Val Asp Val Glu Lys Val Ser Ala
1025   1030   1035   1040

Phe Glu Asn Pro Tyr Val Asp Ala Ile Lys Ser Leu Trp Asn Asp Pro
                1045   1050   1055

Gly Ile Gln Glu Cys Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser Asp
            1060   1065   1070

Ser Thr Lys Tyr Tyr Leu Asn Asp Leu Asp Arg Val Ala Asp Pro Ala
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Tyr Leu Pro Thr Gln Gln Asp Val Leu Arg Val Arg Val Pro Thr Thr
    1090   1095   1100

Gly Ile Ile Glu Tyr Pro Phe Asp Leu Gln Ser Val Ile Phe Arg Met
1105   1110   1115   1120

Val Asp Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys
                1125   1130   1135

Phe Glu Asn Val Thr Ser Ile Met Phe Leu Val Ala Leu Ser Glu Tyr
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Asp Gln Val Leu Val Glu Ser Asp Asn Glu Asn Arg Met Glu Glu Ser
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Lys Ala Leu Phe Arg Thr Ile Ile Thr Tyr Pro Trp Phe Gln Asn Ser
1170 1175 1180

Ser Val Ile Leu Phe Leu Asn Lys Lys Asp Leu Leu Glu Glu Lys Ile
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Met Tyr Ser His Leu Val Asp Tyr Phe Pro Glu Tyr Asp Gly Pro Gln
1205 1210 1215

Arg Asp Ala Gln Ala Ala Arg Glu Phe Ile Leu Lys Met Phe Val Asp
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Leu Asn Pro Asp Ser Asp Lys Ile Ile Tyr Ser His Phe Thr Cys Ala
1235 1240 1245

Thr Asp Thr Glu Asn Ile Arg Phe Val Phe Ala Ala Val Lys Asp Thr
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Ile Leu Gln Leu Asn Leu Lys Asp Cys Gly Leu Phe
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<400> 35

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Val Ala Glu Gly Pro Ala Lys Lys Val Leu Thr Leu Glu Gly Asp Leu
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Val Leu Gly Gly Leu Phe Pro Val His Gln Lys Gly Gly Pro Ala Glu
        35   40   45

Asp Cys Gly Pro Val Asn Glu His Arg Gly Ile Gln Arg Leu Glu Ala

50 55 60

Met Leu Phe Ala Leu Asp Arg Ile Asn Arg Asp Pro His Leu Leu Pro
65 70 75 80

Gly Val Arg Leu Gly Ala His Ile Leu Asp Ser Cys Ser Lys Asp Thr
85 90 95

His Ala Leu Glu Gln Ala Leu Asp Phe Val Arg Ala Ser Leu Ser Arg
100 105 110

Gly Ala Asp Gly Ser Arg His Ile Cys Pro Asp Gly Ser Tyr Ala Thr
115 120 125

His Gly Asp Ala Pro Thr Ala Ile Thr Gly Val Ile Gly Gly Ser Tyr
130 135 140

Ser Asp Val Ser Ile Gln Val Ala Asn Leu Leu Arg Leu Phe Gln Ile
145 150 155 160

Pro Gln Ile Ser Tyr Ala Ser Thr Ser Ala Lys Leu Ser Asp Lys Ser
165 170 175

Arg Tyr Asp Tyr Phe Ala Arg Thr Val Pro Pro Asp Phe Phe Gln Ala
180 185 190

Lys Ala Met Ala Glu Ile Leu Arg Phe Phe Asn Trp Thr Tyr Val Ser
195 200 205

Thr Val Ala Ser Glu Gly Asp Tyr Gly Glu Thr Gly Ile Glu Ala Phe
210 215 220

Glu Leu Glu Ala Arg Ala Arg Asn Ile Cys Val Ala Thr Ser Glu Lys
225 230 235 240

Val Gly Arg Ala Met Ser Arg Ala Ala Phe Glu Gly Val Val Arg Ala
245 250 255

Leu Leu Gln Lys Pro Ser Ala Arg Val Ala Val Leu Phe Thr Arg Ser
260 265 270

Glu Asp Ala Arg Glu Leu Leu Ala Ala Ser Gln Arg Leu Asn Ala Ser
275 280 285

Phe Thr Trp Val Ala Ser Asp Gly Trp Gly Ala Leu Glu Ser Val Val
290 295 300

Ala Gly Ser Glu Gly Ala Ala Glu Gly Ala Ile Thr Ile Glu Leu Ala
305 310 315 320

Ser Tyr Pro Ile Ser Asp Phe Ala Ser Tyr Phe Gln Ser Leu Asp Pro
325 330 335

Trp Asn Asn Ser Arg Asn Pro Trp Phe Arg Glu Phe Trp Glu Gln Arg
340 345 350

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Phe Arg Cys Ser Phe Arg Gln Arg Asp Cys Ala Ala His Ser Leu Arg
        355                 360                 365

Ala Val Pro Phe Glu Gln Glu Ser Lys Ile Met Phe Val Val Asn Ala
    370                 375                 380

Val Tyr Ala Met Ala His Ala Leu His Asn Met His Arg Ala Leu Cys
385                 390                 395                 400

Pro Asn Thr Thr Arg Leu Cys Asp Ala Met Arg Pro Val Asn Gly Arg
                405                 410                 415

Arg Leu Tyr Lys Asp Phe Val Leu Asn Val Lys Phe Asp Ala Pro Phe
            420                 425                 430

Arg Pro Ala Asp Thr His Asn Glu Val Arg Phe Asp Arg Phe Gly Asp
        435                 440                 445

Gly Ile Gly Arg Tyr Asn Ile Phe Thr Tyr Leu Arg Ala Gly Ser Gly
    450                 455                 460

Arg Tyr Arg Tyr Gln Lys Val Gly Tyr Trp Ala Glu Gly Leu Thr Leu
465                 470                 475                 480

Asp Thr Ser Leu Ile Pro Trp Ala Ser Pro Ser Ala Gly Pro Leu Pro
                485                 490                 495

Ala Ser Arg Cys Ser Glu Pro Cys Leu Gln Asn Glu Val Lys Ser Val
            500                 505                 510

Gln Pro Gly Glu Val Cys Cys Trp Leu Cys Ile Pro Cys Gln Pro Tyr
        515                 520                 525

Glu Tyr Arg Leu Asp Glu Phe Thr Cys Ala Asp Cys Gly Leu Gly Tyr
    530                 535                 540

Trp Pro Asn Ala Ser Leu Thr Gly Cys Phe Glu Leu Pro Gln Glu Tyr
545                 550                 555                 560


Ile Arg Trp Gly Asp Ala Trp Ala Val Gly Pro Val Thr Ile Ala Cys
                565                 570                 575

Leu Gly Ala Leu Ala Thr Leu Phe Val Leu Gly Val Phe Val Arg His
            580                 585                 590

Asn Ala Thr Pro Val Val Lys Ala Ser Gly Arg Glu Leu Cys Tyr Ile
        595                 600                 605

Leu Leu Gly Gly Val Phe Leu Cys Tyr Cys Met Thr Phe Ile Phe Ile
    610                 615                 620

Ala Lys Pro Ser Thr Ala Val Cys Thr Leu Arg Arg Leu Gly Leu Gly
625                 630                 635                 640

Thr Ala Phe Ser Val Cys Tyr Ser Ala Leu Leu Thr Lys Thr Asn Arg
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645 650 655

Ile Ala Arg Ile Phe Gly Gly Ala Arg Glu Gly Ala Gln Arg Pro Arg
660 665 670

Phe Ile Ser Pro Ala Ser Gln Val Ala Ile Cys Leu Ala Leu Ile Ser
675 680 685

Gly Gln Leu Leu Ile Val Val Ala Trp Leu Val Val Glu Ala Pro Gly
690 695 700

Thr Gly Lys Glu Thr Ala Pro Glu Arg Arg Glu Val Val Thr Leu Arg
705 710 715 720

Cys Asn His Arg Asp Ala Ser Met Leu Gly Ser Leu Ala Tyr Asn Val
725 730 735

Leu Leu Ile Ala Leu Cys Thr Leu Tyr Ala Phe Lys Thr Arg Lys Cys
740 745 750

Pro Glu Asn Phe Asn Glu Ala Lys Phe Ile Gly Phe Thr Met Tyr Thr
755 760 765

Thr Cys Ile Ile Trp Leu Ala Phe Leu Pro Ile Phe Tyr Val Thr Ser
770 775 780

Ser Asp Tyr Arg Val Gln Thr Thr Thr Met Cys Val Ser Val Ser Leu
785 790 795 800

Ser Gly Ser Val Val Leu Gly Cys Leu Phe Ala Pro Lys Leu His Ile
805 810 815

Ile Leu Phe Gln Pro Gln Lys Asn Thr Ile Glu Glu Val Arg Cys Ser
820 825 830

Thr Ala Ala His Ala Phe Lys Val Ala Ala Arg Ala Thr Leu Arg Arg
835 840 845

Ser Asn Val Ser Arg Lys Arg Ser Ser Ser Leu Gly Gly Ser Thr Gly
850 855 860

Ser Thr Pro Ser Ser Ser Ile Ser Ser Lys Ser Asn Ser Glu Asp Pro
865 870 875 880

Phe Pro Gln Pro Glu Arg Gln Lys Gln Gln Gln Pro Leu Ala Leu Thr
885 890 895

Gln Gln Glu Gln Gln Gln Gln Pro Leu Thr Leu Pro Gln Gln Gln Arg
900 905 910

Ser Gln Gln Gln Pro Arg Cys Lys Gln Lys Val Ile Phe Gly Ser Gly
915 920 925

Thr Val Thr Phe Ser Leu Ser Phe Asp Glu Pro Gln Lys Asn Ala Met
930 935 940

Ala His Gly Asn Ser Thr His Gln Asn Ser Leu Glu Ala Gln Lys Ser
945 950 955 960

Ser Asp Thr Leu Thr Arg His Gln Pro Leu Leu Pro Leu Gln Cys Gly
965 970 975

Glu Thr Asp Leu Asp Leu Thr Val Gln Glu Thr Gly Leu Gln Gly Pro
980 985 990

Val Gly Gly Asp Gln Arg Pro Glu Val Glu Asp Pro Glu Glu Leu Ser
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Pro Ala Leu Val Val Ser Ser Ser Gln Ser Phe Val Ile Ser Gly Gly
1010 1015 1020

Gly Ser Thr Val Thr Glu Asn Val Val Asn Ser
1025 1030 1035

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<220>
<223> Chimeric pmGluR2//CaR*G(qi5

<400> 36

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<400> 37

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Val Leu Gly Gly Leu Phe Pro Val His Gln Lys Gly Gly Pro Ala Glu
        35   40   45

Asp Cys Gly Pro Val Asn Glu His Arg Gly Ile Gln Arg Leu Glu Ala
    50   55   60

Met Leu Phe Ala Leu Asp Arg Ile Asn Arg Asp Pro His Leu Leu Pro
65   70   75   80

Gly Val Arg Leu Gly Ala His Ile Leu Asp Ser Cys Ser Lys Asp Thr
                85   90   95

His Ala Leu Glu Gln Ala Leu Asp Phe Val Arg Ala Ser Leu Ser Arg
            100   105   110

Gly Ala Asp Gly Ser Arg His Ile Cys Pro Asp Gly Ser Tyr Ala Thr
        115   120   125

His Gly Asp Ala Pro Thr Ala Ile Thr Gly Val Ile Gly Gly Ser Tyr
    130   135   140

Ser Asp Val Ser Ile Gln Val Ala Asn Leu Leu Arg Leu Phe Gln Ile
145   150   155   160

Pro Gln Ile Ser Tyr Ala Ser Thr Ser Ala Lys Leu Ser Asp Lys Ser
                165   170   175

Arg Tyr Asp Tyr Phe Ala Arg Thr Val Pro Pro Asp Phe Phe Gln Ala
            180   185   190

Lys Ala Met Ala Glu Ile Leu Arg Phe Phe Asn Trp Thr Tyr Val Ser
        195   200   205

Thr Val Ala Ser Glu Gly Asp Tyr Gly Glu Thr Gly Ile Glu Ala Phe
    210   215   220

Glu Leu Glu Ala Arg Ala Arg Asn Ile Cys Val Ala Thr Ser Glu Lys
225   230   235   240

Val Gly Arg Ala Met Ser Arg Ala Ala Phe Glu Gly Val Val Arg Ala
                245   250   255

Leu Leu Gln Lys Pro Ser Ala Arg Val Ala Val Leu Phe Thr Arg Ser
            260   265   270

Glu Asp Ala Arg Glu Leu Leu Ala Ala Ser Gln Arg Leu Asn Ala Ser
        275   280   285

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Phe Thr Trp Val Ala Ser Asp Gly Trp Gly Ala Leu Glu Ser Val Val
    290                 295                 300

Ala Gly Ser Glu Gly Ala Ala Glu Gly Ala Ile Thr Ile Glu Leu Ala
305                 310                 315                 320

Ser Tyr Pro Ile Ser Asp Phe Ala Ser Tyr Phe Gln Ser Leu Asp Pro
                325                 330                 335

Trp Asn Asn Ser Arg Asn Pro Trp Phe Arg Glu Phe Trp Glu Gln Arg
            340                 345                 350

Phe Arg Cys Ser Phe Arg Gln Arg Asp Cys Ala Ala His Ser Leu Arg
        355                 360                 365

Ala Val Pro Phe Glu Gln Glu Ser Lys Ile Met Phe Val Val Asn Ala
    370                 375                 380

Val Tyr Ala Met Ala His Ala Leu His Asn Met His Arg Ala Leu Cys
385                 390                 395                 400

Pro Asn Thr Thr Arg Leu Cys Asp Ala Met Arg Pro Val Asn Gly Arg
                405                 410                 415

Arg Leu Tyr Lys Asp Phe Val Leu Asn Val Lys Phe Asp Ala Pro Phe
            420                 425                 430

Arg Pro Ala Asp Thr His Asn Glu Val Arg Phe Asp Arg Phe Gly Asp
        435                 440                 445


Gly Ile Gly Arg Tyr Asn Ile Phe Thr Tyr Leu Arg Ala Gly Ser Gly
    450                 455                 460

Arg Tyr Arg Tyr Gln Lys Val Gly Tyr Trp Ala Glu Gly Leu Thr Leu
465                 470                 475                 480

Asp Thr Ser Leu Ile Pro Trp Ala Ser Pro Ser Ala Gly Pro Leu Pro
                485                 490                 495

Ala Ser Arg Cys Ser Glu Pro Cys Leu Gln Asn Glu Val Lys Ser Val
            500                 505                 510

Gln Pro Gly Glu Val Cys Cys Trp Leu Cys Ile Pro Cys Gln Pro Tyr
        515                 520                 525

Glu Tyr Arg Leu Asp Glu Phe Thr Cys Ala Asp Cys Gly Leu Gly Tyr
    530                 535                 540

Trp Pro Asn Ala Ser Leu Thr Gly Cys Phe Glu Leu Pro Gln Glu Tyr
545                 550                 555                 560

Ile Arg Trp Gly Asp Ala Trp Ala Val Gly Pro Val Thr Ile Ala Cys
                565                 570                 575

Leu Gly Ala Leu Ala Thr Leu Phe Val Leu Gly Val Phe Val Arg His
            580                 585                 590
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Asn Ala Thr Pro Val Val Lys Ala Ser Gly Arg Glu Leu Cys Tyr Ile
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Leu Leu Gly Gly Val Phe Leu Cys Tyr Cys Met Thr Phe Ile Phe Ile
610 615 620

Ala Lys Pro Ser Thr Ala Val Cys Thr Leu Arg Arg Leu Gly Leu Gly
625 630 635 640

Thr Ala Phe Ser Val Cys Tyr Ser Ala Leu Leu Thr Lys Thr Asn Arg
645 650 655

Ile Ala Arg Ile Phe Gly Gly Ala Arg Glu Gly Ala Gln Arg Pro Arg
660 665 670

Phe Ile Ser Pro Ala Ser Gln Val Ala Ile Cys Leu Ala Leu Ile Ser
675 680 685

Gly Gln Leu Leu Ile Val Val Ala Trp Leu Val Val Glu Ala Pro Gly
690 695 700

Thr Gly Lys Glu Thr Ala Pro Glu Arg Arg Glu Val Val Thr Leu Arg
705 710 715 720

Cys Asn His Arg Asp Ala Ser Met Leu Gly Ser Leu Ala Tyr Asn Val
725 730 735

Leu Leu Ile Ala Leu Cys Thr Leu Tyr Ala Phe Lys Thr Arg Lys Cys
740 745 750

Pro Glu Asn Phe Asn Glu Ala Lys Phe Ile Gly Phe Thr Met Tyr Thr
755 760 765

Thr Cys Ile Ile Trp Leu Ala Phe Leu Pro Ile Phe Tyr Val Thr Ser
770 775 780

Ser Asp Tyr Arg Val Gln Thr Thr Thr Met Cys Val Ser Val Ser Leu
785 790 795 800

Ser Gly Ser Val Val Leu Gly Cys Leu Phe Ala Pro Lys Leu His Ile
805 810 815

Ile Leu Phe Gln Pro Gln Lys Asn Thr Ile Glu Glu Val Arg Cys Ser
820 825 830

Thr Ala Ala His Ala Phe Lys Val Ala Ala Arg Ala Thr Leu Arg Arg
835 840 845

Ser Asn Val Ser Arg Lys Arg Ser Ser Ser Leu Gly Gly Ser Thr Gly
850 855 860

Ser Thr Pro Ser Ser Ser Ile Ser Ser Lys Ser Asn Ser Glu Asp Pro
865 870 875 880

Phe Pro Gln Pro Glu Arg Gln Lys Gln Gln Gln Pro Leu Ala Leu Thr

885 890 895

Gln Gln Glu Gln Gln Gln Gln Pro Leu Thr Leu Pro Gln Gln Gln Arg
900 905 910

Ser Gln Gln Gln Pro Arg Cys Lys Gln Lys Val Ile Phe Gly Ser Gly
915 920 925

Thr Val Thr Phe Ser Leu Ser Phe Asp Glu Pro Gln Lys Asn Ala Met
930 935 940

Ala His Gly Asn Ser Thr His Gln Asn Ser Leu Glu Ala Gln Lys Ser
945 950 955 960

Ser Asp Thr Leu Thr Arg His Gln Pro Leu Leu Pro Leu Gln Cys Gly
965 970 975

Glu Thr Asp Leu Asp Leu Thr Val Gln Glu Thr Gly Leu Gln Gly Pro
980 985 990

Val Gly Gly Asp Gln Arg Pro Glu Val Glu Asp Pro Glu Glu Leu Ser
995 1000 1005

Pro Ala Leu Val Val Ser Ser Ser Gln Ser Phe Val Ile Ser Gly Gly
1010 1015 1020

Gly Ser Thr Val Thr Glu Asn Val Val Asn Ser Met Thr Leu Glu Ser
1025 1030 1035 1040

Ile Met Ala Cys Cys Leu Ser Glu Glu Ala Lys Glu Ala Arg Arg Ile
1045 1050 1055

Asn Asp Glu Ile Glu Arg Gln Leu Arg Arg Asp Lys Arg Asp Ala Arg
1060 1065 1070

Arg Glu Leu Lys Leu Leu Leu Leu Gly Thr Gly Glu Ser Gly Lys Ser
1075 1080 1085

Thr Phe Ile Lys Gln Met Arg Ile Ile His Gly Ser Gly Tyr Ser Asp
1090 1095 1100

Glu Asp Lys Arg Gly Phe Thr Lys Leu Val Tyr Gln Asn Ile Phe Thr
1105 1110 1115 1120

Ala Met Gln Ala Met Ile Arg Ala Met Asp Thr Leu Lys Ile Pro Tyr
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Lys Tyr Glu His Asn Lys Ala His Ala Gln Leu Val Arg Glu Val Asp
1140 1145 1150

Val Glu Lys Val Ser Ala Phe Glu Asn Pro Tyr Val Asp Ala Ile Lys
1155 1160 1165

Ser Leu Trp Asn Asp Pro Gly Ile Gln Glu Cys Tyr Asp Arg Arg Arg
1170 1175 1180

Glu Tyr Gln Leu Ser Asp Ser Thr Lys Tyr Tyr Leu Asn Asp Leu Asp
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Arg Val Ala Asp Pro Ala Tyr Leu Pro Thr Gln Gln Asp Val Leu Arg
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Ser Val Ile Phe Arg Met Val Asp Val Gly Gly Gln Arg Ser Glu Arg
1235 1240 1245

Arg Lys Trp Ile His Cys Phe Glu Asn Val Thr Ser Ile Met Phe Leu
1250 1255 1260

Val Ala Leu Ser Glu Tyr Asp Gln Val Leu Val Glu Ser Asp Asn Glu
1265 1270 1275 1280

Asn Arg Met Glu Glu Ser Lys Ala Leu Phe Arg Thr Ile Ile Thr Tyr
1285 1290 1295

Pro Trp Phe Gln Asn Ser Ser Val Ile Leu Phe Leu Asn Lys Lys Asp
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Leu Leu Glu Glu Lys Ile Met Tyr Ser His Leu Val Asp Tyr Phe Pro
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Glu Tyr Asp Gly Pro Gln Arg Asp Ala Gln Ala Ala Arg Glu Phe Ile
1330 1335 1340

Leu Lys Met Phe Val Asp Leu Asn Pro Asp Ser Asp Lys Ile Ile Tyr
1345 1350 1355 1360

Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn Ile Arg Phe Val Phe
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Ala Ala Val Lys Asp Thr Ile Leu Gln Leu Asn Leu Lys Asp Cys Gly
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Leu Phe

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<400> 38

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<223> Chimeric hmGluR8/hCaR

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Ser Gln Glu Tyr Ala His Ser Ile Arg Val Asp Gly Asp Ile Ile Leu
35 40 45

Gly Gly Leu Phe Pro Val His Ala Lys Gly Glu Arg Gly Val Pro Cys
50 55 60

Gly Glu Leu Lys Lys Glu Lys Gly Ile His Arg Leu Glu Ala Met Leu
65 70 75 80

Tyr Ala Ile Asp Gln Ile Asn Lys Asp Pro Asp Leu Leu Ser Asn Ile
85 90 95

Thr Leu Gly Val Arg Ile Leu Asp Thr Cys Ser Arg Asp Thr Tyr Ala
100 105 110

Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Glu Lys Asp Ala
115 120 125

Ser Asp Val Lys Cys Ala Asn Gly Asp Pro Pro Ile Phe Thr Lys Pro
130 135 140

Asp Lys Ile Ser Gly Val Ile Gly Ala Ala Ala Ser Ser Val Ser Ile
145 150 155 160

Met Val Ala Asn Ile Leu Arg Leu Phe Lys Ile Pro Gln Ile Ser Tyr
165 170 175

Ala Ser Thr Ala Pro Glu Leu Ser Asp Asn Thr Arg Tyr Asp Phe Phe
180 185 190

Ser Arg Val Val Pro Pro Asp Ser Tyr Gln Ala Gln Ala Met Val Asp
195 200 205

Ile Val Thr Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu Ala Ser Glu
210 215 220

Gly Asn Tyr Gly Glu Ser Gly Val Glu Ala Phe Thr Gln Ile Ser Arg
225 230 235 240

Glu Ile Gly Gly Val Cys Ile Ala Gln Ser Gln Lys Ile Pro Arg Glu
245 250 255

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Pro Arg Pro Gly Glu Phe Glu Lys Ile Ile Lys Arg Leu Leu Glu Thr
            260                 265                 270

Pro Asn Ala Arg Ala Val Ile Met Phe Ala Asn Glu Asp Asp Ile Arg
        275                 280                 285

Arg Ile Leu Glu Ala Ala Lys Lys Leu Asn Gln Ser Gly His Phe Leu
    290                 295                 300

Trp Ile Gly Ser Asp Ser Trp Gly Ser Lys Ile Ala Pro Val Tyr Gln
305                 310                 315                 320

Gln Glu Glu Ile Ala Glu Gly Ala Val Thr Ile Leu Pro Lys Arg Ala
                325                 330                 335

Ser Ile Asp Gly Phe Asp Arg Tyr Phe Arg Ser Arg Thr Leu Ala Asn
            340                 345                 350

Asn Arg Arg Asn Val Trp Phe Ala Glu Phe Trp Glu Glu Asn Phe Gly
        355                 360                 365

Cys Lys Leu Gly Ser His Gly Lys Arg Asn Ser His Ile Lys Lys Cys
    370                 375                 380

Thr Gly Leu Glu Arg Ile Ala Arg Asp Ser Ser Tyr Glu Gln Glu Gly
385                 390                 395                 400

Lys Val Gln Phe Val Ile Asp Ala Val Tyr Ser Met Ala Tyr Ala Leu
                405                 410                 415

His Asn Met His Lys Asp Leu Cys Pro Gly Tyr Ile Gly Leu Cys Pro
            420                 425                 430

Arg Met Ser Thr Ile Asp Gly Lys Glu Leu Leu Gly Tyr Ile Arg Ala
        435                 440                 445

Val Asn Phe Asn Gly Ser Ala Gly Thr Pro Val Thr Phe Asn Glu Asn
    450                 455                 460

Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe Gln Tyr Gln Ile Thr Asn
465                 470                 475                 480

Lys Ser Thr Glu Tyr Lys Val Ile Gly His Trp Thr Asn Gln Leu His
                485                 490                 495

Leu Lys Val Glu Asp Met Gln Trp Ala His Arg Glu His Thr His Pro
            500                 505                 510

Ala Ser Val Cys Ser Leu Pro Cys Lys Pro Gly Glu Arg Lys Lys Thr
        515                 520                 525

Val Lys Gly Val Pro Cys Cys Trp His Cys Glu Arg Cys Glu Gly Tyr
    530                 535                 540

Asn Tyr Gln Val Asp Glu Leu Ser Cys Glu Leu Cys Pro Leu Asp Gln
545                 550                 555                 560
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Arg Pro Asn Met Asn Arg Thr Gly Cys Gln Leu Ile Pro Ile Ile Lys
                565                 570                 575

Leu Glu Trp His Ser Pro Trp Ala Val Val Pro Val Phe Val Ala Ile
            580                 585                 590

Leu Gly Ile Ile Ala Thr Thr Phe Val Ile Val Thr Phe Val Arg Tyr
        595                 600                 605

Asn Asp Thr Pro Ile Val Arg Ala Ser Gly Arg Glu Leu Ser Tyr Val
    610                 615                 620

Leu Leu Thr Gly Ile Phe Leu Cys Tyr Ser Ile Thr Phe Leu Met Ile
625                 630                 635                 640

Ala Ala Pro Asp Thr Ile Ile Cys Ser Phe Arg Arg Val Phe Leu Gly
                645                 650                 655

Leu Gly Met Cys Phe Ser Tyr Ala Ala Leu Leu Thr Lys Thr Asn Arg
            660                 665                 670

Ile His Arg Ile Phe Glu Gln Gly Lys Lys Ser Val Thr Ala Pro Lys
        675                 680                 685

Phe Ile Ser Pro Ala Ser Gln Leu Val Ile Thr Phe Ser Leu Ile Ser
    690                 695                 700

Val Gln Leu Leu Gly Val Phe Val Trp Phe Val Val Asp Pro Pro His
705                 710                 715                 720

Ile Ile Ile Asp Tyr Gly Glu Gln Arg Thr Leu Asp Pro Glu Lys Ala
                725                 730                 735

Arg Gly Val Leu Lys Cys Asp Ile Ser Asp Leu Ser Leu Ile Cys Ser
            740                 745                 750

Leu Gly Tyr Ser Ile Leu Leu Met Val Thr Cys Thr Val Tyr Ala Ile
        755                 760                 765

Lys Thr Arg Gly Val Pro Glu Thr Phe Asn Glu Ala Lys Pro Ile Gly
    770                 775                 780

Phe Thr Met Tyr Thr Thr Cys Ile Ile Trp Leu Ala Phe Ile Pro Ile
785                 790                 795                 800

Phe Phe Gly Thr Ala Gln Ser Ala Glu Lys Met Tyr Ile Gln Thr Thr
                805                 810                 815

Thr Leu Thr Val Ser Met Ser Leu Ser Ala Ser Val Ser Leu Gly Met
            820                 825                 830

Leu Tyr Met Pro Lys Val Tyr Ile Ile Ile Phe His Pro Glu Gln Asn
        835                 840                 845

Thr Ile Glu Glu Val Arg Cys Ser Thr Ala Ala His Ala Phe Lys Val
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850 855 860

Ala Ala Arg Ala Thr Leu Arg Arg Ser Asn Val Ser Arg Lys Arg Ser
865 870 875 880

Ser Ser Leu Gly Gly Ser Thr Gly Ser Thr Pro Ser Ser Ser Ile Ser
885 890 895

Ser Lys Ser Asn Ser Glu Asp Pro Phe Pro Gln Pro Glu Arg Gln Lys
900 905 910

Gln Gln Gln Pro Leu Ala Leu Thr Gln Gln Glu Gln Gln Gln Gln Pro
915 920 925

Leu Thr Leu Pro Gln Gln Gln Arg Ser Gln Gln Gln Pro Arg Cys Lys
930 935 940

Gln Lys Val Ile Phe Gly Ser Gly Thr Val Thr Phe Ser Leu Ser Phe
945 950 955 960

Asp Glu Pro Gln Lys Asn Ala Met Ala His Gly Asn Ser Thr His Gln
965 970 975

Asn Ser Leu Glu Ala Gln Lys Ser Ser Asp Thr Leu Thr Arg His Gln
980 985 990

Pro Leu Leu Pro Leu Gln Cys Gly Glu Thr Asp Leu Asp Leu Thr Val
995 1000 1005

Gln Glu Thr Gly Leu Gln Gly Pro Val Gly Gly Asp Gln Arg Pro Glu
1010 1015 1020

Val Glu Asp Pro Glu Glu Leu Ser Pro Ala Leu Val Val Ser Ser Ser
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Gln Ser Phe Val Ile Ser Gly Gly Gly Ser Thr Val Thr Glu Asn Val
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Val Asn Ser

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<211> 4257
<212> DNA
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<220>
<223> Chimeric mGluR8//CaR*G(qi5

<400> 40

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<212> PRT
<213> Artificial Sequence

<220>
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<400> 41

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35 40 45

Gly Gly Leu Phe Pro Val His Ala Lys Gly Glu Arg Gly Val Pro Cys
50 55 60

Gly Glu Leu Lys Lys Glu Lys Gly Ile His Arg Leu Glu Ala Met Leu
65 70 75 80

Tyr Ala Ile Asp Gln Ile Asn Lys Asp Pro Asp Leu Leu Ser Asn Ile
85 90 95

Thr Leu Gly Val Arg Ile Leu Asp Thr Cys Ser Arg Asp Thr Tyr Ala
100 105 110

Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Glu Lys Asp Ala
115 120 125

Ser Asp Val Lys Cys Ala Asn Gly Asp Pro Pro Ile Phe Thr Lys Pro
130 135 140

Asp Lys Ile Ser Gly Val Ile Gly Ala Ala Ala Ser Ser Val Ser Ile
145 150 155 160

Met Val Ala Asn Ile Leu Arg Leu Phe Lys Ile Pro Gln Ile Ser Tyr
165 170 175

Ala Ser Thr Ala Pro Glu Leu Ser Asp Asn Thr Arg Tyr Asp Phe Phe
180 185 190

Ser Arg Val Val Pro Pro Asp Ser Tyr Gln Ala Gln Ala Met Val Asp
195 200 205

Ile Val Thr Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu Ala Ser Glu
210 215 220

Gly Asn Tyr Gly Glu Ser Gly Val Glu Ala Phe Thr Gln Ile Ser Arg
225 230 235 240

Glu Ile Gly Gly Val Cys Ile Ala Gln Ser Gln Lys Ile Pro Arg Glu
245 250 255

Pro Arg Pro Gly Glu Phe Glu Lys Ile Ile Lys Arg Leu Leu Glu Thr
260 265 270

Pro Asn Ala Arg Ala Val Ile Met Phe Ala Asn Glu Asp Asp Ile Arg
275 280 285

Arg Ile Leu Glu Ala Ala Lys Lys Leu Asn Gln Ser Gly His Phe Leu
290 295 300

Trp Ile Gly Ser Asp Ser Trp Gly Ser Lys Ile Ala Pro Val Tyr Gln
305 310 315 320

Gln Glu Glu Ile Ala Glu Gly Ala Val Thr Ile Leu Pro Lys Arg Ala
325 330 335

Ser Ile Asp Gly Phe Asp Arg Tyr Phe Arg Ser Arg Thr Leu Ala Asn
340 345 350

Asn Arg Arg Asn Val Trp Phe Ala Glu Phe Trp Glu Glu Asn Phe Gly
355 360 365

Cys Lys Leu Gly Ser His Gly Lys Arg Asn Ser His Ile Lys Lys Cys
370 375 380

Thr Gly Leu Glu Arg Ile Ala Arg Asp Ser Ser Tyr Glu Gln Glu Gly
385 390 395 400

Lys Val Gln Phe Val Ile Asp Ala Val Tyr Ser Met Ala Tyr Ala Leu
405 410 415

His Asn Met His Lys Asp Leu Cys Pro Gly Tyr Ile Gly Leu Cys Pro
420 425 430

Arg Met Ser Thr Ile Asp Gly Lys Glu Leu Leu Gly Tyr Ile Arg Ala
435 440 445

Val Asn Phe Asn Gly Ser Ala Gly Thr Pro Val Thr Phe Asn Glu Asn
450 455 460

Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe Gln Tyr Gln Ile Thr Asn
465 470 475 480

Lys Ser Thr Glu Tyr Lys Val Ile Gly His Trp Thr Asn Gln Leu His
485 490 495

Leu Lys Val Glu Asp Met Gln Trp Ala His Arg Glu His Thr His Pro
500 505 510

Ala Ser Val Cys Ser Leu Pro Cys Lys Pro Gly Glu Arg Lys Lys Thr
515 520 525

Val Lys Gly Val Pro Cys Cys Trp His Cys Glu Arg Cys Glu Gly Tyr
530 535 540

Asn Tyr Gln Val Asp Glu Leu Ser Cys Glu Leu Cys Pro Leu Asp Gln
545 550 555 560

Arg Pro Asn Met Asn Arg Thr Gly Cys Gln Leu Ile Pro Ile Ile Lys
565 570 575

Leu Glu Trp His Ser Pro Trp Ala Val Val Pro Val Phe Val Ala Ile
580 585 590

Leu Gly Ile Ile Ala Thr Thr Phe Val Ile Val Thr Phe Val Arg Tyr
595 600 605

Asn Asp Thr Pro Ile Val Arg Ala Ser Gly Arg Glu Leu Ser Tyr Val
610 615 620

Leu Leu Thr Gly Ile Phe Leu Cys Tyr Ser Ile Thr Phe Leu Met Ile
625 630 635 640

Ala Ala Pro Asp Thr Ile Ile Cys Ser Phe Arg Arg Val Phe Leu Gly
645 650 655

Leu Gly Met Cys Phe Ser Tyr Ala Ala Leu Leu Thr Lys Thr Asn Arg
660 665 670

Ile His Arg Ile Phe Glu Gln Gly Lys Lys Ser Val Thr Ala Pro Lys
675 680 685

Phe Ile Ser Pro Ala Ser Gln Leu Val Ile Thr Phe Ser Leu Ile Ser
690 695 700

Val Gln Leu Leu Gly Val Phe Val Trp Phe Val Val Asp Pro Pro His
705 710 715 720

Ile Ile Ile Asp Tyr Gly Glu Gln Arg Thr Leu Asp Pro Glu Lys Ala
725 730 735

Arg Gly Val Leu Lys Cys Asp Ile Ser Asp Leu Ser Leu Ile Cys Ser
740 745 750

Leu Gly Tyr Ser Ile Leu Leu Met Val Thr Cys Thr Val Tyr Ala Ile
755 760 765

Lys Thr Arg Gly Val Pro Glu Thr Phe Asn Glu Ala Lys Pro Ile Gly
770 775 780

Phe Thr Met Tyr Thr Thr Cys Ile Ile Trp Leu Ala Phe Ile Pro Ile
785 790 795 800

Phe Phe Gly Thr Ala Gln Ser Ala Glu Lys Met Tyr Ile Gln Thr Thr
805 810 815

Thr Leu Thr Val Ser Met Ser Leu Ser Ala Ser Val Ser Leu Gly Met
820 825 830

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Ser Ser Leu Gly Gly Ser Thr Gly Ser Thr Pro Ser Ser Ser Ile Ser
885 890 895

Ser Lys Ser Asn Ser Glu Asp Pro Phe Pro Gln Pro Glu Arg Gln Lys
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Gln Gln Gln Pro Leu Ala Leu Thr Gln Gln Glu Gln Gln Gln Gln Pro
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930 935 940

Gln Lys Val Ile Phe Gly Ser Gly Thr Val Thr Phe Ser Leu Ser Phe
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Asp Glu Pro Gln Lys Asn Ala Met Ala His Gly Asn Ser Thr His Gln
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Asn Ser Leu Glu Ala Gln Lys Ser Ser Asp Thr Leu Thr Arg His Gln
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Pro Leu Leu Pro Leu Gln Cys Gly Glu Thr Asp Leu Asp Leu Thr Val
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Val Glu Leu Ala Ile Glu Gln Ile Arg Asn Glu Ser Leu Leu Arg Pro
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Tyr Phe Leu Asp Leu Arg Leu Tyr Asp Thr Glu Cys Asp Asn Ala Lys
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Ser Glu Val Arg Asn Asp Leu Thr Gly Val Leu Tyr Gly Glu Asp Ile
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Glu Ile Ser Asp Thr Glu Ser Phe Ser Asn Asp Pro Cys Thr Ser Val
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Trp Trp Glu Gln Val His Thr Glu Ala Asn Ser Ser Arg Cys Leu Arg
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Lys Asn Leu Leu Ala Ala Met Glu Gly Tyr Ile Gly Val Asp Phe Glu
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Pro Leu Ser Ser Lys Gln Ile Lys Thr Ile Ser Gly Lys Thr Pro Gln
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Gln Tyr Glu Arg Glu Tyr Asn Asn Lys Arg Ser Gly Val Gly Pro Ser
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Lys Phe His Gly Tyr Ala Tyr Asp Gly Ile Trp Val Ile Ala Lys Thr
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Phe Arg Asn Gly Glu Arg Met Gly Thr Ile Lys Phe Thr Gln Phe Gln
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Asp Ser Arg Glu Val Lys Val Gly Glu Tyr Asn Ala Val Ala Asp Thr
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Leu Tyr Ser Ile Leu Ser Ala Leu Thr Ile Leu Gly Met Ile Met Ala
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Ser Ala Phe Leu Phe Phe Asn Ile Lys Asn Arg Asn Gln Lys Leu Ile
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Lys Met Ser Ser Pro Tyr Met Asn Asn Leu Ile Ile Leu Gly Gly Met
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Arg Val His Ala Ile Phe Lys Asn Val Lys Met Lys Lys Lys Ile Ile
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Lys Asp Gln Lys Leu Leu Val Ile Val Gly Gly Met Leu Leu Ile Asp
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Val Glu Lys Tyr Ser Met Glu Pro Asp Pro Ala Gly Arg Asp Ile Ser
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Gln Asp Thr Pro Glu Lys Thr Thr Tyr Ile Lys Gln Asn His Tyr Gln
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Glu Leu Asn Asp Ile Leu Asn Leu Gly Asn Phe Thr Glu Ser Thr Asp
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Gly Gly Lys Ala Ile Leu Lys Asn His Leu Asp Gln Asn Pro Gln Leu
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Asp Ile Asn Ser Pro Glu His Ile Gln Arg Arg Leu Ser Leu Gln Leu
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Pro Ile Leu His His Ala Tyr Leu Pro Ser Ile Gly Gly Val Asp Ala
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Ser Cys Val Ser Pro Cys Val Ser Pro Thr Ala Ser Pro Arg His Arg
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His Val Pro Pro Ser Phe Arg Val Met Val Ser Gly Leu Ala Ala Ala
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ggaccccaga gagatgccca ggcagcccga gaattcattc tgaagatgtt cgtggacctg    3840
aacccagaca gtgacaaaat tatctactcc cacttcacgt gcgccacaga caccgagaat    3900
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<400> 45

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Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
            20                  25                  30

Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
        35                  40                  45

Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
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Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
65 70 75 80

Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
85 90 95

Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val
100 105 110

Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp
115 120 125

Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Ile
130 135 140

Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn
145 150 155 160

Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe
165 170 175

Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val
180 185 190

Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp
195 200 205

Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln
210 215 220

Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile
225 230 235 240

Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala
245 250 255

Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro
260 265 270

Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro
275 280 285

Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp
290 295 300

Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr
305 310 315 320

Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu
325 330 335

Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys
340 345 350

Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu
355 360 365

Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe
370 375 380

Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp
385 390 395 400

Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr
405 410 415

Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro
420 425 430

Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu
435 440 445

Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe
450 455 460

Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala
465 470 475 480

Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu
485 490 495

Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala
500 505 510

Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp
515 520 525

Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly
530 535 540

Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu
545 550 555 560

Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp
565 570 575

Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe
580 585 590

Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val
595 600 605

Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn
610 615 620

Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala
625 630 635 640

Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg
645 650 655

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Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu
            660                 665                 670

Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val
        675                 680                 685

His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr
    690                 695                 700

Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met
705                 710                 715                 720

Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg
                725                 730                 735

Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val
            740                 745                 750

Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met Asn Thr
        755                 760                 765

Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly
    770                 775                 780

Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn
785                 790                 795                 800

Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys
                805                 810                 815

Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala
            820                 825                 830

Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr
        835                 840                 845

Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly
    850                 855                 860

Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly Ser Ser Thr
865                 870                 875                 880

Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg
                885                 890                 895

Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu
            900                 905                 910

Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro
        915                 920                 925

Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro Pro Glu
    930                 935                 940

Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr
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945 950 955 960

Lys Ala Ala Ala Met Thr Leu Glu Ser Ile Met Ala Cys Cys Leu Ser
965 970 975

Glu Glu Ala Lys Glu Ala Arg Arg Ile Asn Asp Glu Ile Glu Arg Gln
980 985 990

Leu Arg Arg Asp Lys Arg Asp Ala Arg Arg Glu Leu Lys Leu Leu Leu
995 1000 1005

Leu Gly Thr Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg
1010 1015 1020

Ile Ile His Gly Ser Gly Tyr Ser Asp Glu Asp Lys Arg Gly Phe Thr
1025 1030 1035 1040

Lys Leu Val Tyr Gln Asn Ile Phe Thr Ala Met Gln Ala Met Ile Arg
1045 1050 1055

Ala Met Asp Thr Leu Lys Ile Pro Tyr Lys Tyr Glu His Asn Lys Ala
1060 1065 1070

His Ala Gln Leu Val Arg Glu Val Asp Val Glu Lys Val Ser Ala Phe
1075 1080 1085

Glu Asn Pro Tyr Val Asp Ala Ile Lys Ser Leu Trp Asn Asp Pro Gly
1090 1095 1100

Ile Gln Glu Cys Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser Asp Ser
1105 1110 1115 1120

Thr Lys Tyr Tyr Leu Asn Asp Leu Asp Arg Val Ala Asp Pro Ala Tyr
1125 1130 1135

Leu Pro Thr Gln Gln Asp Val Leu Arg Val Arg Val Pro Thr Thr Gly
1140 1145 1150

Ile Ile Glu Tyr Pro Phe Asp Leu Gln Ser Val Ile Phe Arg Met Val
1155 1160 1165

Asp Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe
1170 1175 1180

Glu Asn Val Thr Ser Ile Met Phe Leu Val Ala Leu Ser Glu Tyr Asp
1185 1190 1195 1200

Gln Val Leu Val Glu Ser Asp Asn Glu Asn Arg Met Glu Glu Ser Lys
1205 1210 1215

Ala Leu Phe Arg Thr Ile Ile Thr Tyr Pro Trp Phe Gln Asn Ser Ser
1220 1225 1230

Val Ile Leu Phe Leu Asn Lys Lys Asp Leu Leu Glu Glu Lys Ile Met
1235 1240 1245

Tyr Ser His Leu Val Asp Tyr Phe Pro Glu Tyr Asp Gly Pro Gln Arg
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Asp Ala Gln Ala Ala Arg Glu Phe Ile Leu Lys Met Phe Val Asp Leu
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Asn Pro Asp Ser Asp Lys Ile Ile Tyr Ser His Phe Thr Cys Ala Thr
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Asp Thr Glu Asn Ile Arg Phe Val Phe Ala Ala Val Lys Asp Thr Ile
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Leu Gln Leu Asn Leu Lys Gly Cys Gly Leu Tyr
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Val Leu Gly Gly Leu Phe Pro Val His Gln Lys Gly Gly Pro Ala Glu
35 40 45

Asp Cys Gly Pro Val Asn Glu His Arg Gly Ile Gln Arg Leu Glu Ala
50 55 60

Met Leu Phe Ala Leu Asp Arg Ile Asn Arg Asp Pro His Leu Leu Pro
65 70 75 80

Gly Val Arg Leu Gly Ala His Ile Leu Asp Ser Cys Ser Lys Asp Thr
85 90 95

His Ala Leu Glu Gln Ala Leu Asp Phe Val Arg Ala Ser Leu Ser Arg
100 105 110

Gly Ala Asp Gly Ser Arg His Ile Cys Pro Asp Gly Ser Tyr Ala Thr
115 120 125

His Gly Asp Ala Pro Thr Ala Ile Thr Gly Val Ile Gly Gly Ser Tyr
130 135 140

Ser Asp Val Ser Ile Gln Val Ala Asn Leu Leu Arg Leu Phe Gln Ile
145 150 155 160

Pro Gln Ile Ser Tyr Ala Ser Thr Ser Ala Lys Leu Ser Asp Lys Ser
165 170 175

Arg Tyr Asp Tyr Phe Ala Arg Thr Val Pro Pro Asp Phe Phe Gln Ala
180 185 190

Lys Ala Met Ala Glu Ile Leu Arg Phe Phe Asn Trp Thr Tyr Val Ser
195 200 205

Thr Val Ala Ser Glu Gly Asp Tyr Gly Glu Thr Gly Ile Glu Ala Phe
210 215 220

Glu Leu Glu Ala Arg Ala Arg Asn Ile Cys Val Ala Thr Ser Glu Lys
225 230 235 240

Val Gly Arg Ala Met Ser Arg Ala Ala Phe Glu Gly Val Val Arg Ala
245 250 255

Leu Leu Gln Lys Pro Ser Ala Arg Val Ala Val Leu Phe Thr Arg Ser
260 265 270

Glu Asp Ala Arg Glu Leu Leu Ala Ala Ser Gln Arg Leu Asn Ala Ser
275 280 285

Phe Thr Trp Val Ala Ser Asp Gly Trp Gly Ala Leu Glu Ser Val Val
290 295 300

Ala Gly Ser Glu Gly Ala Ala Glu Gly Ala Ile Thr Ile Glu Leu Ala

305 310 315 320

Ser Tyr Pro Ile Ser Asp Phe Ala Ser Tyr Phe Gln Ser Leu Asp Pro
325 330 335

Trp Asn Asn Ser Arg Asn Pro Trp Phe Arg Glu Phe Trp Glu Gln Arg
340 345 350

Phe Arg Cys Ser Phe Arg Gln Arg Asp Cys Ala Ala His Ser Leu Arg
355 360 365

Ala Val Pro Phe Glu Gln Glu Ser Lys Ile Met Phe Val Val Asn Ala
370 375 380

Val Tyr Ala Met Ala His Ala Leu His Asn Met His Arg Ala Leu Cys
385 390 395 400

Pro Asn Thr Thr Arg Leu Cys Asp Ala Met Arg Pro Val Asn Gly Arg
405 410 415

Arg Leu Tyr Lys Asp Phe Val Leu Asn Val Lys Phe Asp Ala Pro Phe
420 425 430

Arg Pro Ala Asp Thr His Asn Glu Val Arg Phe Asp Arg Phe Gly Asp
435 440 445

Gly Ile Gly Arg Tyr Asn Ile Phe Thr Tyr Leu Arg Ala Gly Ser Gly
450 455 460

Arg Tyr Arg Tyr Gln Lys Val Gly Tyr Trp Ala Glu Gly Leu Thr Leu
465 470 475 480

Asp Thr Ser Leu Ile Pro Trp Ala Ser Pro Ser Ala Gly Pro Leu Pro
485 490 495

Ala Ser Arg Cys Ser Glu Pro Cys Leu Gln Asn Glu Val Lys Ser Val
500 505 510

Gln Pro Gly Glu Val Cys Cys Trp Leu Cys Ile Pro Cys Gln Pro Tyr
515 520 525

Glu Tyr Arg Leu Asp Glu Phe Thr Cys Ala Asp Cys Gly Leu Gly Tyr
530 535 540

Trp Pro Asn Ala Ser Leu Thr Gly Cys Phe Glu Leu Pro Gln Glu Tyr
545 550 555 560

Ile Arg Trp Gly Asp Ala Trp Ala Val Gly Pro Val Thr Ile Ala Cys
565 570 575

Leu Gly Ala Leu Ala Thr Leu Phe Val Leu Gly Val Phe Val Arg His
580 585 590

Asn Ala Thr Pro Val Val Lys Ala Ser Gly Arg Glu Leu Cys Tyr Ile
595 600 605

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Ala Lys Pro Ser Thr Ala Val Cys Thr Leu Arg Arg Leu Gly Leu Gly
625                 630                 635                 640

Thr Ala Phe Ser Val Cys Tyr Ser Ala Leu Leu Thr Lys Thr Asn Arg
                645                 650                 655

Ile Ala Arg Ile Phe Gly Gly Ala Arg Glu Gly Ala Gln Arg Pro Arg
            660                 665                 670

Phe Ile Ser Pro Ala Ser Gln Val Ala Ile Cys Leu Ala Leu Ile Ser
        675                 680                 685

Gly Gln Leu Leu Ile Val Val Ala Trp Leu Val Val Glu Ala Pro Gly
    690                 695                 700

Thr Gly Lys Glu Thr Ala Pro Glu Arg Arg Glu Val Val Thr Leu Arg
705                 710                 715                 720

Cys Asn His Arg Asp Ala Ser Met Leu Gly Ser Leu Ala Tyr Asn Val
                725                 730                 735

Leu Leu Ile Ala Leu Cys Thr Leu Tyr Ala Phe Lys Thr Arg Lys Cys
            740                 745                 750

Pro Glu Asn Phe Asn Glu Ala Lys Phe Ile Gly Phe Thr Met Tyr Thr
        755                 760                 765

Thr Cys Ile Ile Trp Leu Ala Phe Leu Pro Ile Phe Tyr Val Thr Ser
    770                 775                 780

Ser Asp Tyr Arg Val Gln Thr Thr Thr Met Cys Val Ser Val Ser Leu
785                 790                 795                 800

Ser Gly Ser Val Val Leu Gly Cys Leu Phe Ala Pro Lys Leu His Ile
                805                 810                 815

Ile Leu Phe Gln Pro Gln Lys Asn Thr Ile Glu Glu Val Arg Cys Ser
            820                 825                 830

Thr Ala Ala His Ala Phe Lys Val Ala Ala Arg Ala Thr Leu Arg Arg
        835                 840                 845

Ser Asn Val Ser Arg Lys Arg Ser Ser Ser Leu Gly Gly Ser Thr Gly
    850                 855                 860

Ser Thr Pro Ser Ser Ser Ile Ser Ser Lys Ser Asn Ser Glu Asp Pro
865                 870                 875                 880

Phe Pro Gln Pro Glu Arg Gln Lys Gln Gln Gln Pro Leu Ala Leu Thr
                885                 890                 895

Gln Gln Glu Gln Gln Gln Gln Pro Leu Thr Leu Pro Gln Gln Gln Arg
            900                 905                 910
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Ser Gln Gln Gln Pro Arg Cys Lys Gln Lys Val Ile Phe Gly Ser Gly
        915                 920                 925

Thr Val Thr Phe Ser Leu Ser Phe Asp Glu Pro Gln Lys Asn Ala Met
    930                 935                 940

Ala His Gly Asn Ser Thr His Gln Asn Ser Leu Glu Ala Gln Lys Ser
945                 950                 955                 960

Ser Asp Thr Leu Thr Arg His Gln Pro Leu Leu Pro Leu Gln Cys Gly
                965                 970                 975

Glu Thr Asp Leu Asp Leu Thr Val Gln Glu Thr Gly Leu Gln Gly Pro
            980                 985                 990

Val Gly Gly Asp Gln Arg Pro Glu Val Glu Asp Pro Glu Glu Leu Ser
        995                 1000                1005

Pro Ala Leu Val Val Ser Ser Ser Gln Ser Phe Val Ile Ser Gly Gly
    1010                1015                1020

Gly Ser Thr Val Thr Glu Asn Val Val Asn Ser Ala Ala Ala Met Thr
1025                1030                1035                1040

Leu Glu Ser Ile Met Ala Cys Cys Leu Ser Glu Glu Ala Lys Glu Ala
                1045                1050                1055

Arg Arg Ile Asn Asp Glu Ile Glu Arg Gln Leu Arg Arg Asp Lys Arg
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Asp Ala Arg Arg Glu Leu Lys Leu Leu Leu Leu Gly Thr Gly Glu Ser
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Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile Ile His Gly Ser Gly
    1090                1095                1100

Tyr Ser Asp Glu Asp Lys Arg Gly Phe Thr Lys Leu Val Tyr Gln Asn
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Ile Phe Thr Ala Met Gln Ala Met Ile Arg Ala Met Asp Thr Leu Lys
                1125                1130                1135

Ile Pro Tyr Lys Tyr Glu His Asn Lys Ala His Ala Gln Leu Val Arg
            1140                1145                1150

Glu Val Asp Val Glu Lys Val Ser Ala Phe Glu Asn Pro Tyr Val Asp
        1155                1160                1165

Ala Ile Lys Ser Leu Trp Asn Asp Pro Gly Ile Gln Glu Cys Tyr Asp
    1170                1175                1180

Arg Arg Arg Glu Tyr Gln Leu Ser Asp Ser Thr Lys Tyr Tyr Leu Asn
1185                1190                1195                1200

Asp Leu Asp Arg Val Ala Asp Pro Ala Tyr Leu Pro Thr Gln Gln Asp
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Val Leu Arg Val Arg Val Pro Thr Thr Gly Ile Ile Glu Tyr Pro Phe
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Ser Glu Arg Arg Lys Trp Ile His Cys Phe Glu Asn Val Thr Ser Ile
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Met Phe Leu Val Ala Leu Ser Glu Tyr Asp Gln Val Leu Val Glu Ser
1265 1270 1275 1280

Asp Asn Glu Asn Arg Met Glu Glu Ser Lys Ala Leu Phe Arg Thr Ile
1285 1290 1295

Ile Thr Tyr Pro Trp Phe Gln Asn Ser Ser Val Ile Leu Phe Leu Asn
1300 1305 1310

Lys Lys Asp Leu Leu Glu Glu Lys Ile Met Tyr Ser His Leu Val Asp
1315 1320 1325

Tyr Phe Pro Glu Tyr Asp Gly Pro Gln Arg Asp Ala Gln Ala Ala Arg
1330 1335 1340

Glu Phe Ile Leu Lys Met Phe Val Asp Leu Asn Pro Asp Ser Asp Lys
1345 1350 1355 1360

Ile Ile Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn Ile Arg
1365 1370 1375

Phe Val Phe Ala Ala Val Lys Asp Thr Ile Leu Gln Leu Asn Leu Lys
1380 1385 1390

Asp Cys Gly Leu Phe
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Leu Thr Ala Lys Phe Tyr Trp Ile Leu Thr Met Met Gln Arg Thr His
20 25 30
Ser Gln Glu Tyr Ala His Ser Ile Arg Ile Asp Gly Asp Ile Thr Leu
35 40 45
Gly Gly Leu Phe Pro Val His Gly Arg Gly Ser Glu Gly Lys Pro Cys
50 55 60
Gly Glu Leu Lys Lys Glu Lys Gly Ile His Arg Leu Glu Ala Met Leu
65 70 75 80

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Phe Ala Leu Asp Arg Ile Asn Asn Asp Pro Asp Leu Leu Pro Asn Ile
                85                  90                  95
Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp Thr His Ala
            100                 105                 110
Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Glu Lys Asp Gly
        115                 120                 125
Thr Glu Val Arg Cys Gly Ser Gly Gly Pro Pro Ile Ile Thr Lys Pro
    130                 135                 140
Glu Arg Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser Val Ser Ile
145                 150                 155                 160
Met Val Ala Asn Ile Leu Arg Leu Phe Lys Ile Pro Gln Ile Ser Tyr
                165                 170                 175
Ala Ser Thr Ala Pro Asp Leu Ser Asp Asn Ser Arg Tyr Asp Phe Phe
            180                 185                 190
Ser Arg Val Val Pro Ser Asp Thr Tyr Gln Ala Gln Ala Met Val Asp
        195                 200                 205
Ile Val Arg Ala Leu Lys Trp Asn Tyr Val Ser Thr Val Ala Ser Glu
    210                 215                 220
Gly Ser Tyr Gly Glu Ser Gly Val Glu Ala Phe Ile Gln Lys Ser Arg
225                 230                 235                 240
Glu Asp Gly Gly Val Cys Ile Ala Gln Ser Val Lys Ile Pro Arg Glu
                245                 250                 255
Pro Lys Ala Gly Glu Phe Asp Lys Ile Ile Arg Arg Leu Leu Glu Thr
            260                 265                 270
Ser Asn Ala Arg Ala Val Ile Ile Phe Ala Asn Glu Asp Asp Ile Arg
        275                 280                 285
Arg Val Leu Glu Ala Ala Arg Arg Ala Asn Gln Thr Gly His Phe Phe
    290                 295                 300
Trp Met Gly Ser Asp Ser Trp Gly Ser Lys Ile Ala Pro Val Leu His
305                 310                 315                 320
Leu Glu Glu Val Ala Glu Gly Ala Val Thr Ile Leu Pro Lys Arg Met
                325                 330                 335
Ser Val Arg Gly Phe Asp Arg Tyr Phe Ser Ser Arg Thr Leu Asp Asn
            340                 345                 350
Asn Arg Arg Asn Ile Trp Phe Ala Glu Phe Trp Glu Asp Asn Phe His
        355                 360                 365
Cys Lys Leu Ser Arg His Ala Leu Lys Lys Gly Ser His Val Lys Lys
    370                 375                 380
Cys Thr Asn Arg Glu Arg Ile Gly Gln Asp Ser Ala Tyr Glu Gln Glu
385                 390                 395                 400
Gly Lys Val Gln Phe Val Ile Asp Ala Val Tyr Ala Met Gly His Ala
                405                 410                 415
Leu His Ala Met His Arg Asp Leu Cys Pro Gly Arg Val Gly Leu Cys
            420                 425                 430
Pro Arg Met Asp Pro Val Asp Gly Thr Gln Leu Leu Lys Tyr Ile Arg
        435                 440                 445
Asn Val Asn Phe Ser Gly Ile Ala Gly Asn Pro Val Thr Phe Asn Glu
    450                 455                 460
Asn Gly Asp Ala Pro Gly Arg Tyr Asp Ile Tyr Gln Tyr Gln Leu Arg
465                 470                 475                 480
Asn Asp Ser Ala Glu Tyr Lys Val Ile Gly Ser Trp Thr Asp His Leu
                485                 490                 495
His Leu Arg Ile Glu Arg Met His Trp Pro Gly Ser Gly Gln Gln Leu
            500                 505                 510
Pro Arg Ser Ile Cys Ser Leu Pro Cys Gln Pro Gly Glu Arg Lys Lys
        515                 520                 525
Thr Val Lys Gly Met Pro Cys Cys Trp His Cys Glu Pro Cys Thr Gly
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530 535 540
Tyr Gln Tyr Gln Val Asp Arg Tyr Thr Cys Lys Thr Cys Pro Tyr Asp
545 550 555 560
Met Arg Pro Thr Glu Asn Arg Thr Gly Cys Arg Pro Ile Pro Ile Ile
565 570 575
Lys Leu Glu Trp Gly Ser Pro Trp Ala Val Leu Pro Leu Phe Leu Ala
580 585 590
Val Val Gly Ile Ala Ala Thr Leu Phe Val Val Ile Thr Phe Val Arg
595 600 605
Tyr Asn Asp Thr Pro Ile Val Lys Ala Ser Gly Arg Glu Leu Ser Tyr
610 615 620
Val Leu Leu Ala Gly Ile Phe Leu Cys Tyr Ala Thr Thr Phe Leu Met
625 630 635 640
Ile Ala Glu Pro Asp Leu Gly Thr Cys Ser Leu Arg Arg Ile Phe Leu
645 650 655
Gly Leu Gly Met Ser Ile Ser Tyr Ala Ala Leu Leu Thr Lys Thr Asn
660 665 670
Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys Arg Ser Val Ser Ala Pro
675 680 685
Arg Phe Ile Ser Pro Ala Ser Gln Leu Ala Ile Thr Phe Ser Leu Ile
690 695 700
Ser Leu Gln Leu Leu Gly Ile Cys Val Trp Phe Val Val Asp Pro Ser
705 710 715 720
His Ser Val Val Asp Phe Gln Asp Gln Arg Thr Leu Asp Pro Arg Phe
725 730 735
Arg Val Leu Lys Cys Asp Ile Ser Asp Leu Ser Leu Ile Cys Leu Leu
740 745 750
Gly Tyr Ser Met Leu Leu Met Val Thr Cys Thr Val Tyr Ala Ile Lys
755 760 765
Thr Arg Gly Val Pro Glu Thr Phe Asn Glu Ala Lys Pro Ile Gly Phe
770 775 780
Thr Met Tyr Thr Thr Cys Ile Val Trp Leu Ala Phe Ile Pro Ile Phe
785 790 795 800
Phe Gly Thr Ser Gln Ser Ala Asp Lys Leu Tyr Ile Gln Thr Thr Thr
805 810 815
Leu Thr Val Ser Val Ser Leu Ser Ala Ser Val Ser Leu Gly Met Leu
820 825 830
Tyr Met Pro Lys Val Tyr Ile Ile Leu Phe His Pro Glu Gln Asn Val
835 840 845
Pro Lys Arg Lys Arg Ser Leu Lys Ala Val Val Thr Ala Ala Thr Met
850 855 860
Ser Asn Lys Phe Thr Gln Lys Gly Asn Phe Arg Pro Asn Gly Glu Ala
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Lys Ser Glu Leu Cys Glu Asn Leu Glu Ala Pro Ala Thr Lys Gln Thr
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Tyr Val Thr Tyr Thr Asn His Ala Ile
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Ser Gln Glu Tyr Ala His Ser Ile Arg Ile Asp Gly Asp Ile Thr Leu
35 40 45
Gly Gly Leu Phe Pro Val His Gly Arg Gly Ser Glu Gly Lys Pro Cys
50 55 60
Gly Glu Leu Lys Lys Glu Lys Gly Ile His Arg Leu Glu Ala Met Leu
65 70 75 80
Phe Ala Leu Asp Arg Ile Asn Asn Asp Pro Asp Leu Leu Pro Asn Ile
85 90 95
Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp Thr His Ala
100 105 110
Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Glu Lys Asp Gly
115 120 125
Thr Glu Val Arg Cys Gly Ser Gly Gly Pro Pro Ile Ile Thr Lys Pro
130 135 140
Glu Arg Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser Val Ser Ile
145 150 155 160
Met Val Ala Asn Ile Leu Arg Leu Phe Lys Ile Pro Gln Ile Ser Tyr
165 170 175
Ala Ser Thr Ala Pro Asp Leu Ser Asp Asn Ser Arg Tyr Asp Phe Phe
180 185 190
Ser Arg Val Val Pro Ser Asp Thr Tyr Gln Ala Gln Ala Met Val Asp
195 200 205
Ile Val Arg Ala Leu Lys Trp Asn Tyr Val Ser Thr Val Ala Ser Glu
210 215 220
Gly Ser Tyr Gly Glu Ser Gly Val Glu Ala Phe Ile Gln Lys Ser Arg
225 230 235 240
Glu Asp Gly Gly Val Cys Ile Ala Gln Ser Val Lys Ile Pro Arg Glu
245 250 255
Pro Lys Ala Gly Glu Phe Asp Lys Ile Ile Arg Arg Leu Leu Glu Thr
260 265 270
Ser Asn Ala Arg Ala Val Ile Ile Phe Ala Asn Glu Asp Asp Ile Arg
275 280 285
Arg Val Leu Glu Ala Ala Arg Arg Ala Asn Gln Thr Gly His Phe Phe
290 295 300
Trp Met Gly Ser Asp Ser Trp Gly Ser Lys Ile Ala Pro Val Leu His
305 310 315 320
Leu Glu Glu Val Ala Glu Gly Ala Val Thr Ile Leu Pro Lys Arg Met
325 330 335
Ser Val Arg Gly Phe Asp Arg Tyr Phe Ser Ser Arg Thr Leu Asp Asn
340 345 350
Asn Arg Arg Asn Ile Trp Phe Ala Glu Phe Trp Glu Asp Asn Phe His
355 360 365
Cys Lys Leu Ser Arg His Ala Leu Lys Lys Gly Ser His Val Lys Lys
370 375 380
Cys Thr Asn Arg Glu Arg Ile Gly Gln Asp Ser Ala Tyr Glu Gln Glu
385 390 395 400
Gly Lys Val Gln Phe Val Ile Asp Ala Val Tyr Ala Met Gly His Ala
405 410 415
Leu His Ala Met His Arg Asp Leu Cys Pro Gly Arg Val Gly Leu Cys
420 425 430
Pro Arg Met Asp Pro Val Asp Gly Thr Gln Leu Leu Lys Tyr Ile Arg
435 440 445
Asn Val Asn Phe Ser Gly Ile Ala Gly Asn Pro Val Thr Phe Asn Glu
450 455 460
Asn Gly Asp Ala Pro Gly Arg Tyr Asp Ile Tyr Gln Tyr Gln Leu Arg

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465                 470                 475                 480
Asn Asp Ser Ala Glu Tyr Lys Val Ile Gly Ser Trp Thr Asp His Leu
                485                 490                 495
His Leu Arg Ile Glu Arg Met His Trp Pro Gly Ser Gly Gln Gln Leu
            500                 505                 510
Pro Arg Ser Ile Cys Ser Leu Pro Cys Gln Pro Gly Glu Arg Lys Lys
        515                 520                 525
Thr Val Lys Gly Met Pro Cys Cys Trp His Cys Glu Pro Cys Thr Gly
    530                 535                 540
Tyr Gln Tyr Gln Val Asp Arg Tyr Thr Cys Lys Thr Cys Pro Tyr Asp
545                 550                 555                 560
Met Arg Pro Thr Glu Asn Arg Thr Gly Cys Arg Pro Ile Pro Ile Ile
                565                 570                 575
Lys Leu Glu Trp Gly Ser Pro Trp Ala Val Leu Pro Leu Phe Leu Ala
            580                 585                 590
Val Val Gly Ile Ala Ala Thr Leu Phe Val Val Ile Thr Phe Val Arg
        595                 600                 605
Tyr Asn Asp Thr Pro Ile Val Lys Ala Ser Gly Arg Glu Leu Ser Tyr
    610                 615                 620
Val Leu Leu Ala Gly Ile Phe Leu Cys Tyr Ala Thr Thr Phe Leu Met
625                 630                 635                 640
Ile Ala Glu Pro Asp Leu Gly Thr Cys Ser Leu Arg Arg Ile Phe Leu
                645                 650                 655
Gly Leu Gly Met Ser Ile Ser Tyr Ala Ala Leu Leu Thr Lys Thr Asn
            660                 665                 670
Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys Arg Ser Val Ser Ala Pro
        675                 680                 685
Arg Phe Ile Ser Pro Ala Ser Gln Leu Ala Ile Thr Phe Ser Leu Ile
    690                 695                 700
Ser Leu Gln Leu Leu Gly Ile Cys Val Trp Phe Val Val Asp Pro Ser
705                 710                 715                 720
His Ser Val Val Asp Phe Gln Asp Gln Arg Thr Leu Asp Pro Arg Phe
                725                 730                 735
Arg Val Leu Lys Cys Asp Ile Ser Asp Leu Ser Leu Ile Cys Leu Leu
            740                 745                 750
Gly Tyr Ser Met Leu Leu Met Val Thr Cys Thr Val Tyr Ala Ile Lys
        755                 760                 765
Thr Arg Gly Val Pro Glu Thr Phe Asn Glu Ala Lys Pro Ile Gly Phe
    770                 775                 780
Thr Met Tyr Thr Thr Cys Ile Val Trp Leu Ala Phe Ile Pro Ile Phe
785                 790                 795                 800
Phe Gly Thr Ser Gln Ser Ala Asp Lys Leu Tyr Ile Gln Thr Thr Thr
                805                 810                 815
Leu Thr Val Ser Val Ser Leu Ser Ala Ser Val Ser Leu Gly Met Leu
            820                 825                 830
Tyr Met Pro Lys Val Tyr Ile Ile Leu Phe His Pro Glu Gln Asn Thr
        835                 840                 845
Ile Glu Glu Val Arg Cys Ser Thr Ala Ala His Ala Phe Lys Val Ala
    850                 855                 860
Ala Arg Ala Thr Leu Arg Arg Ser Asn Val Ser Arg Lys Arg Ser Ser
865                 870                 875                 880
Ser Leu Gly Gly Ser Thr Gly Ser Thr Pro Ser Ser Ser Ile Ser Ser
                885                 890                 895
Lys Ser Asn Ser Glu Asp Pro Phe Pro Gln Pro Glu Arg Gln Lys Gln
            900                 905                 910
Gln Gln Pro Leu Ala Leu Thr Gln Gln Glu Gln Gln Gln Gln Pro Leu
        915                 920                 925
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Thr Leu Pro Gln Gln Gln Arg Ser Gln Gln Gln Pro Arg Cys Lys Gln
930 935 940

Lys Val Ile Phe Gly Ser Gly Thr Val Thr Phe Ser Leu Ser Phe Asp
945 950 955 960

Glu Pro Gln Lys Asn Ala Met Ala His Gly Asn Ser Thr His Gln Asn
965 970 975

Ser Leu Glu Ala Gln Lys Ser Ser Asp Thr Leu Thr Arg His Gln Pro
980 985 990

Leu Leu Pro Leu Gln Cys Gly Glu Thr Asp Leu Asp Leu Thr Val Gln
995 1000 1005

Glu Thr Gly Leu Gln Gly Pro Val Gly Gly Asp Gln Arg Pro Glu Val
1010 1015 1020

Glu Asp Pro Glu Glu Leu Ser Pro Ala Leu Val Val Ser Ser Ser Gln
1025 1030 1035 1040

Ser Phe Val Ile Ser Gly Gly Gly Ser Thr Val Thr Glu Asn Val Val
1045 1050 1055

Asn Ser Ala Ala Ala Met Thr Leu Glu Ser Ile Met Ala Cys Cys Leu
1060 1065 1070

Ser Glu Glu Ala Lys Glu Ala Arg Arg Ile Asn Asp Glu Ile Glu Arg
1075 1080 1085

Gln Leu Arg Arg Asp Lys Arg Asp Ala Arg Arg Glu Leu Lys Leu Leu
1090 1095 1100

Leu Leu Gly Thr Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met
1105 1110 1115 1120

Arg Ile Ile His Gly Ser Gly Tyr Ser Asp Glu Asp Lys Arg Gly Phe
1125 1130 1135

Thr Lys Leu Val Tyr Gln Asn Ile Phe Thr Ala Met Gln Ala Met Ile
1140 1145 1150

Arg Ala Met Asp Thr Leu Lys Ile Pro Tyr Lys Tyr Glu His Asn Lys
1155 1160 1165

Ala His Ala Gln Leu Val Arg Glu Val Asp Val Glu Lys Val Ser Ala
1170 1175 1180

Phe Glu Asn Pro Tyr Val Asp Ala Ile Lys Ser Leu Trp Asn Asp Pro
1185 1190 1195 1200

Gly Ile Gln Glu Cys Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser Asp
1205 1210 1215

Ser Thr Lys Tyr Tyr Leu Asn Asp Leu Asp Arg Val Ala Asp Pro Ala
1220 1225 1230

Tyr Leu Pro Thr Gln Gln Asp Val Leu Arg Val Arg Val Pro Thr Thr
1235 1240 1245

Gly Ile Ile Glu Tyr Pro Phe Asp Leu Gln Ser Val Ile Phe Arg Met
1250 1255 1260

Val Asp Val Gly Gly Gln Arg Ser Arg Lys Trp Ile His Cys Phe Glu
1265 1270 1275 1280

Asn Val Thr Ser Ile Met Phe Leu Val Ser Glu Tyr Asp Gln Val Leu
1285 1290 1295

Val Glu Ser Asp Asn Glu Asn Arg Met Glu Glu Ser Lys Ala Leu Phe
1300 1305 1310

Arg Thr Ile Ile Thr Tyr Pro Trp Phe Gln Asn Ser Ser Val Ile Leu
1315 1320 1325

Phe Leu Asn Lys Lys Asp Leu Leu Glu Glu Lys Ile Met Tyr Ser His
1330 1335 1340

Leu Val Asp Tyr Phe Pro Glu Tyr Asp Gly Pro Gln Arg Asp Ala Gln
1345 1350 1355 1360

Ala Ala Arg Glu Phe Ile Leu Lys Met Phe Val Asp Leu Asn Pro Asp
1365 1370 1375

Ser Asp Lys Ile Ile Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu

1380 1385 1390
Asn Ile Arg Phe Val Phe Ala Ala Val Lys Asp Thr Ile Leu Gln Leu
1395 1400 1405
Asn Leu Lys Asp Cys Gly Leu Phe
1410 1415

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20 25 30
Ser Gln Glu Tyr Ala His Ser Ile Arg Val Asp Gly Asp Ile Ile Leu
35 40 45
Gly Gly Leu Phe Pro Val His Ala Lys Gly Glu Arg Gly Val Pro Cys
50 55 60
Gly Glu Leu Lys Lys Glu Lys Gly Ile His Arg Leu Glu Ala Met Leu
65 70 75 80
Tyr Ala Ile Asp Gln Ile Asn Lys Asp Pro Asp Leu Leu Ser Asn Ile
85 90 95
Thr Leu Gly Val Arg Ile Leu Asp Thr Cys Ser Arg Asp Thr Tyr Ala
100 105 110
Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Glu Lys Asp Ala
115 120 125
Ser Asp Val Lys Cys Ala Asn Gly Asp Pro Pro Ile Phe Thr Lys Pro
130 135 140
Asp Lys Ile Ser Gly Val Ile Gly Ala Ala Ala Ser Ser Val Ser Ile
145 150 155 160
Met Val Ala Asn Ile Leu Arg Leu Phe Lys Ile Pro Gln Ile Ser Tyr
165 170 175
Ala Ser Thr Ala Pro Glu Leu Ser Asp Asn Thr Arg Tyr Asp Phe Phe
180 185 190
Ser Arg Val Val Pro Pro Asp Ser Tyr Gln Ala Gln Ala Met Val Asp
195 200 205
Ile Val Thr Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu Ala Ser Glu
210 215 220
Gly Asn Tyr Gly Glu Ser Gly Val Glu Ala Phe Thr Gln Ile Ser Arg
225 230 235 240
Glu Ile Gly Gly Val Cys Ile Ala Gln Ser Gln Lys Ile Pro Arg Glu
245 250 255
Pro Arg Pro Gly Glu Phe Glu Lys Ile Ile Lys Arg Leu Leu Glu Thr
260 265 270
Pro Asn Ala Arg Ala Val Ile Met Phe Ala Asn Glu Asp Asp Ile Arg
275 280 285
Arg Ile Ala Ala Lys Lys Leu Asn Gln Ser Gly His Phe Leu Trp Ile
290 295 300
Gly Ser Asp Ser Trp Gly Ser Lys Ile Ala Pro Val Tyr Gln Gln Glu
305 310 315 320
Glu Ile Ala Glu Gly Ala Val Thr Ile Leu Pro Lys Arg Ala Ser Ile
325 330 335
Asp Gly Phe Asp Arg Tyr Phe Arg Ser Arg Thr Leu Ala Asn Asn Arg
340 345 350

Arg Asn Val Trp Phe Ala Glu Phe Trp Glu Glu Asn Phe Gly Cys Lys
355 360 365
Leu Gly Ser His Gly Lys Arg Asn Ser His Ile Lys Lys Cys Thr Gly
370 375 380
Leu Glu Arg Ile Ala Arg Asp Ser Ser Tyr Glu Gln Glu Gly Lys Val
385 390 395 400
Gln Phe Val Ile Asp Ala Val Tyr Ser Met Ala Tyr Ala Leu His Asn
405 410 415
Met His Lys Asp Leu Cys Pro Gly Tyr Ile Gly Leu Cys Pro Arg Met
420 425 430
Ser Thr Ile Asp Gly Lys Glu Leu Leu Gly Tyr Ile Arg Ala Val Asn
435 440 445
Phe Asn Gly Ser Ala Gly Thr Pro Val Thr Phe Asn Glu Asn Gly Asp
450 455 460
Ala Pro Gly Arg Tyr Asp Ile Phe Gln Tyr Gln Ile Thr Asn Lys Ser
465 470 475 480
Thr Glu Tyr Lys Val Ile Gly His Trp Thr Asn Gln Leu His Leu Lys
485 490 495
Val Glu Asp Met Gln Trp Ala His Arg Glu His Thr His Pro Ala Ser
500 505 510
Val Cys Ser Leu Pro Cys Lys Pro Gly Glu Arg Lys Lys Thr Val Lys
515 520 525
Gly Val Pro Cys Cys Trp His Cys Glu Arg Cys Glu Gly Tyr Asn Tyr
530 535 540
Gln Val Asp Glu Leu Ser Cys Glu Leu Cys Pro Leu Asp Gln Arg Pro
545 550 555 560
Asn Met Asn Arg Thr Gly Cys Gln Leu Ile Pro Ile Ile Lys Leu Glu
565 570 575
Trp His Ser Pro Trp Ala Val Val Pro Val Phe Val Ala Ile Leu Gly
580 585 590
Ile Ile Ala Thr Thr Phe Val Ile Val Thr Phe Val Arg Tyr Asn Asp
595 600 605
Thr Pro Ile Val Arg Ala Ser Gly Arg Glu Leu Ser Tyr Val Leu Leu
610 615 620
Thr Gly Ile Phe Leu Cys Ile Thr Phe Leu Met Ile Ala Ala Pro Asp
625 630 635 640
Thr Ile Ile Cys Ser Phe Arg Arg Val Phe Leu Gly Leu Gly Met Cys
645 650 655
Phe Ser Tyr Ala Ala Leu Leu Thr Lys Thr Asn Arg Ile His Arg Ile
660 665 670
Phe Glu Gln Gly Lys Lys Ser Val Thr Ala Pro Lys Phe Ile Ser Pro
675 680 685
Ala Ser Gln Leu Val Ile Thr Phe Ser Leu Ile Ser Val Gln Leu Leu
690 695 700
Gly Val Phe Val Trp Phe Val Val Asp Pro Pro His Ile Ile Ile Asp
705 710 715 720
Tyr Gly Glu Gln Arg Thr Leu Asp Pro Glu Lys Arg Val Leu Lys Cys
725 730 735
Asp Ile Ser Asp Leu Ser Leu Ile Cys Ser Leu Gly Tyr Ser Ile Leu
740 745 750
Leu Met Val Thr Cys Thr Val Tyr Ala Ile Lys Thr Arg Gly Val Pro
755 760 765
Glu Thr Phe Asn Glu Ala Lys Pro Ile Gly Phe Thr Met Tyr Thr Thr
770 775 780
Cys Ile Ile Trp Leu Ala Phe Ile Pro Ile Phe Phe Gly Thr Ala Gln
785 790 795 800
Ser Ala Glu Lys Met Tyr Ile Gln Thr Thr Thr Leu Thr Val Ser Met

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                805                 810                 815
Ser Leu Ser Ala Ser Val Ser Leu Gly Met Leu Tyr Met Pro Lys Val
            820                 825                 830
Tyr Ile Ile Ile Phe His Pro Glu Gln Asn Thr Ile Glu Glu Val Arg
        835                 840                 845
Cys Ser Thr Ala Ala His Ala Phe Lys Val Ala Ala Arg Ala Thr Leu
    850                 855                 860
Arg Arg Ser Asn Val Ser Arg Lys Arg Ser Ser Ser Leu Gly Gly Ser
865                 870                 875                 880
Thr Gly Ser Thr Pro Ser Ser Ser Ile Ser Ser Lys Ser Asn Ser Glu
                885                 890                 895
Asp Pro Phe Pro Gln Pro Glu Arg Gln Lys Gln Gln Gln Pro Leu Ala
            900                 905                 910
Leu Thr Gln Gln Glu Gln Gln Gln Gln Pro Leu Thr Leu Pro Gln Gln
        915                 920                 925
Gln Arg Ser Gln Gln Gln Pro Arg Cys Lys Gln Lys Val Ile Phe Gly
    930                 935                 940
Ser Gly Thr Val Thr Phe Ser Leu Ser Phe Asp Glu Pro Gln Lys Asn
945                 950                 955                 960
Ala Met Ala His Gly Asn Ser Thr His Gln Asn Ser Leu Glu Ala Gln
                965                 970                 975
Lys Ser Ser Asp Thr Leu Thr Arg His Gln Pro Leu Leu Pro Leu Gln
            980                 985                 990
Cys Gly Glu Thr Asp Leu Asp Leu Thr Val Gln Glu Thr Gly Leu Gln
        995                 1000                1005
Gly Pro Val Gly Gly Asp Gln Arg Pro Glu Val Glu Asp Pro Glu Glu
    1010                1015                1020
Leu Ser Pro Ala Leu Val Val Ser Ser Ser Gln Ser Phe Val Ile Ser
1025                1030                1035                1040
Gly Gly Gly Ser Thr Val Thr Glu Asn Val Val Asn Ser Ala Ala Ala
                1045                1050                1055
Met Thr Leu Glu Ser Ile Met Ala Cys Cys Leu Ser Glu Glu Ala Lys
            1060                1065                1070
Glu Ala Arg Arg Ile Asn Asp Glu Ile Glu Arg Gln Leu Arg Arg Asp
        1075                1080                1085
Lys Arg Asp Ala Arg Arg Glu Leu Lys Leu Leu Leu Leu Gly Thr Gly
    1090                1095                1100
Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile Ile His Gly
1105                1110                1115                1120
Ser Gly Tyr Ser Asp Glu Asp Lys Arg Gly Phe Thr Lys Leu Val Tyr
                1125                1130                1135
Gln Asn Ile Phe Thr Ala Met Gln Ala Met Ile Arg Ala Met Asp Thr
            1140                1145                1150
Leu Lys Ile Pro Tyr Lys Tyr Glu His Asn Lys Ala His Ala Gln Leu
        1155                1160                1165
Val Arg Glu Val Asp Val Glu Lys Val Ser Ala Phe Glu Asn Pro Tyr
    1170                1175                1180
Val Asp Ala Ile Lys Ser Leu Trp Asn Asp Pro Gly Ile Gln Glu Cys
1185                1190                1195                1200
Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser Asp Ser Thr Lys Tyr Tyr
                1205                1210                1215
Leu Asn Asp Leu Asp Arg Val Ala Asp Pro Ala Tyr Leu Pro Thr Gln
            1220                1225                1230
Gln Asp Val Leu Arg Val Arg Val Pro Thr Thr Gly Ile Ile Glu Tyr
        1235                1240                1245
Pro Phe Asp Leu Gln Ser Val Ile Phe Arg Met Val Asp Val Gly Gly
    1250                1255                1260
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Gln Arg Ser Arg Lys Trp Ile His Cys Phe Glu Asn Val Thr Ser Ile
1265   1270   1275   1280
Met Phe Leu Val Ser Glu Tyr Asp Gln Val Leu Val Glu Ser Asp Asn
                1285   1290   1295
Glu Asn Arg Met Glu Glu Ser Lys Ala Leu Phe Arg Thr Ile Ile Thr
            1300   1305   1310
Tyr Pro Trp Phe Gln Asn Ser Ser Val Ile Leu Phe Leu Asn Lys Lys
        1315   1320   1325
Asp Leu Leu Glu Glu Lys Ile Met Tyr Ser His Leu Val Asp Tyr Phe
    1330   1335   1340
Pro Glu Tyr Asp Gly Pro Gln Arg Asp Ala Gln Ala Ala Arg Glu Phe
1345   1350   1355   1360
Ile Leu Lys Met Phe Val Asp Leu Asn Pro Asp Ser Asp Lys Ile Ile
                1365   1370   1375
Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn Ile Arg Phe Val
            1380   1385   1390
Phe Ala Ala Val Lys Asp Thr Ile Leu Gln Leu Asn Leu Lys Asp Cys
        1395   1400   1405
Gly Leu Phe
    1410